BLAST Basic Local Alignment Search Tool

Job Title: X70683:H.sapiens mRNA for SOX-4 protein

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Please, try our new design!

BLASTN 2.2.18+

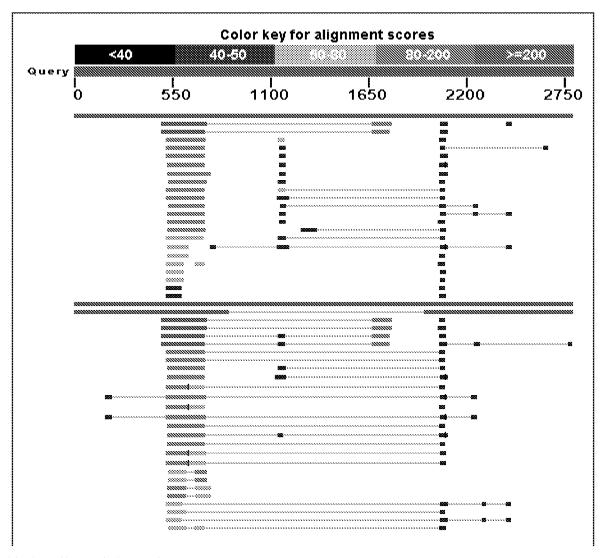
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 7WFMZ732012 Database: human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters

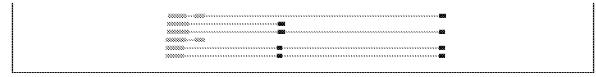
Genome View

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= gi|36552|emb|X70683.1|HSSOX4M H.sapiens mRNA for SOX-4 protein Length=2797

Distribution of 270 Blast Hits on the Query Sequence





Distance tree of results NEW

Legend for links to other resources: Will UniGene GEO Gene Structure Will Map Viewer

Sequences producing significant alignments: (Click headers to sort columns)

Transcripts

Transcripts						
NM_003107.2	Homo sapiens SRY (sex determining region Y)-box 5012 $4 \pmod{50}$, mRNA	5012	99%	0.0	99%	G
NM_003108.3	Homo sapiens SRY (sex determining region Y)-box 309 11 (SOX11), mRNA	440	13%	1e-80	86%	
NM_006943.2	Homo sapiens SRY (sex determining region Y)-box 291 12 (SOX12), mRNA	422	12%	3e-75	88%	
NM_006941.3	Homo sapiens SRY (sex determining region Y)-box 167		7%	7e-38	77%	
NM_000346.2	Homo sapiens SRY (sex determining region Y)-box 156 9 (campomelic dysplasia, autosomal sex- reversal) (SOX9), mRNA			1e-34	75%	[C]
NM_007084.2	Homo sapiens SRY (sex determining region Y)-box 140 21 (SOX21), mRNA	140	7%	1e-29	74%	G
NM_006942.1	Homo sapiens SRY (sex determining region Y)-box 129 15 (SOX15), mRNA	129	7%	2e-26	74%	
NM_014587.2	Homo sapiens SRY (sex determining region Y)-box 127 8 (SOX8), mRNA	127	8%	7e-26	71%	
NM_031439.2	Homo sapiens SRY (sex determining region Y)-box 113 7 (SOX7), mRNA	113	7%	1e-21	71%	G
NM_018419.2	Homo sapiens SRY (sex determining region Y)-box 107 18 (SOX18), mRNA	107	7%	6e-20	71%	
NM_004189.2	Homo sapiens SRY (sex determining region Y)-box 104 14 (SOX14), mRNA	104	7%	8e-19	71%	
NM_022454.3	Homo sapiens SRY (sex determining region Y)-box 100 17 (SOX17), mRNA	100	7%	9e-18	71%	
NM_005634.2	Homo sapiens SRY (sex determining region Y)-box 100 3 (SOX3), mRNA	100	7%	9e-18	71%	
NM_005986.2	Homo sapiens SRY (sex determining region Y)-box 96.9 1 (SOX1), mRNA	96.9	7%	1e-16	70%	a
NM_003106.2	Homo sapiens SRY (sex determining region Y)-box 91.5 2 (SOX2), mRNA	91.5	7%	5e-15	69%	
NM_005686.2	Homo sapiens SRY (sex determining region Y)-box 78.8 13 (SOX13), mRNA	78.8	7%	3e-11	70%	
XM_001713691.1	PREDICTED: Homo sapiens hypothetical protein 64.4 LOC100130809 (LOC100130809), mRNA	64.4	4%	7e-07	74%	C
NM_003140.1	Homo sapiens sex determining region Y (SRY), 64.4 mRNA	64.4	4%	7e-07	74%	
NM_152989.2	Homo sapiens SRY (sex determining region Y)-box 57.2 5 (SOX5), transcript variant 2, mRNA	57.2	3%	1e-04	73%	
NM_006940.4	Homo sapiens SRY (sex determining region Y)-box 57.2 5 (SOX5), transcript variant 1, mRNA	57.2	3%	1e-04	73%	
NM_178010.1	Homo sapiens SRY (sex determining region Y)-box 57.2 5 (SOX5), transcript variant 3, mRNA	57.2	3%	1e-04	73%	
NM_052876.2	Homo sapiens BTB (POZ) domain containing 14B 51.8 (BTBD14B), mRNA	51.8	1%	0.004	89%	
NM_033326.2	Homo sapiens SRY (sex determining region Y)-box 50.0 6 (SOX6), transcript variant 2, mRNA	50.0	3%	0.014	72%	
NM_017508.1	Homo sapiens SRY (sex determining region Y)-box 50.0 6 (SOX6), transcript variant 1, mRNA	50.0	38	0.014	72%	

XM_001132155.2	(Protein AF-6) (LOC730031), mRNA		46.4		0.18	88%	G
NM_001040001.1	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 1, mRNA		46.4	1%	0.18	88%	
NM_001040000.1	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 2, mRNA	46.4	46.4	1%	0.18	88%	G
NM_005936.2	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 3, mRNA	46.4	46.4	1%	0.18	88%	<u>G</u>
ΝМ_015156.2	Homo sapiens REST corepressor 1 (RCOR1), mRNA	44.6	44.6	1%	0.62	83%	G
Genomic sequen	ces [show first]						
NT_007592.14	Homo sapiens chromosome 6 genomic contig, reference assembly	5012	5094	998	0.0	99%	
NW_001838973.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188126)	1570	3057	60%	0.0	100%	
NW_001838765.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188139)	309	440	13%	1e-80	86%	
NT_005334.15	Homo sapiens chromosome 2 genomic contig, reference assembly	309	440	13%	1e-80	86%	
NW_001838652.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on HuRef SCAF_1103279188366)	291	601	13%	3e-75	88%	
NT_011387.8	Homo sapiens chromosome 20 genomic contig, reference assembly	291	601	13%	3e-75	88%	
NW_001838084.2	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188152)	140	182	8%	1e-29	90%	
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	140	182	88	1e-29	90%	
NW_001838403.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on HuRef SCAF_1103279188371)		129	7%	2e-26	74%	
NT_010718.15	Homo sapiens chromosome 17 genomic contig, reference assembly		129	7%	2e-26	74%	
NW_001838454.2	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on HuRef SCAF_1103279188168)	104	246	8%	8e-19	90%	
NW_001838884.2	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188385)	104	366	11%	8e-19	92%	
NT_010641.15	Homo sapiens chromosome 17 genomic contig, reference assembly	104	163	7%	8e-19	78%	
NT_005612.15	Homo sapiens chromosome 3 genomic contig, reference assembly	104	448	11%	8e-19	92%	
NW_001842405.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188404)	100	141	8%	9e-18	87%	
NT_011786.15	Homo sapiens chromosome X genomic contig, reference assembly	100	223	10%	9e-18	92%	
NT_027140.6	Homo sapiens chromosome 13 genomic contig, reference assembly		137		1e-16	92%	
NW_001838745.1	Homo sapiens chromosome 22 genomic contig,	95.1	255	98	4e-16	96%	

	alternate assembly (based on HuRef SCAF_1103279188372)		
NT_011520.11	Homo sapiens chromosome 22 genomic contig, reference assembly	95.1 255 9%	4e-16 96%
NW_001839122.2	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188150)	87.8 141 6%	6e-14 87%
NT_077531.3	Homo sapiens chromosome 8 genomic contig, reference assembly	87.8 141 6%	6e-14 87%
NW_001838339.2	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on HuRef SCAF_1103279188181)	86.0 139 7%	2e-13 77%
NT_037887.4	Homo sapiens chromosome 16 genomic contig, reference assembly	86.0 139 7%	2e-13 77%
NW_001838533.2	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on HuRef SCAF_1103279188157)	77.0 335 6%	1e-10 100%
NW_001838085.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188104)	77.0 117 4%	1e-10 92%
NT_004487.18	Homo sapiens chromosome 1 genomic contig, reference assembly	77.0 376 6%	1e-10 100%
NW_001839132.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188282)	66.2 285 7%	2e-07 92%
NT_008183.18	Homo sapiens chromosome 8 genomic contig, reference assembly	66.2 328 7%	2e-07 92%
NW_001842422.1	Homo sapiens chromosome Y genomic contig, alternate assembly (based on HuRef SCAF_1103279188414)	64.4 108 5%	7e-07 84%
NT_011896.9	Homo sapiens chromosome Y genomic contig, reference assembly	64.4 192 7%	7e-07 87%
NT_011333.5	Homo sapiens chromosome 20 genomic contig, reference assembly	62.6 116 6%	2e-06 79%
NW_001838052.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188408)	57.2 140 5%	1e-04 96%
NT_009714.16	Homo sapiens chromosome 12 genomic contig, reference assembly	57.2 181 5%	1e-04 96%
NW_001838671.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on HuRef SCAF_1103279188118)	53.6 53.6 2%	0.001 79%
NW_001838954.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188298)	51.8 180 5%	0.004 90%
NT_011295.10	Homo sapiens chromosome 19 genomic contig, reference assembly	51.8 92.7 2%	0.004 96%
NT_023133.12	Homo sapiens chromosome 5 genomic contig, reference assembly	51.8 180 5%	0.004 90%
NW_001838022.2	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on HuRef SCAF_1103279188392)	50.0 131 5%	0.014 92%
NW_001838468.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on HuRef SCAF_1103279188038)	50.0 50.0 1%	0.014 87%
NW_001838951.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188395)	50.0 94.5 1%	0.014 87%
NW_001838865.2	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188138)	50.0 50.0 1%	0.014 87%

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NT_006576.15	Homo sapiens chromosome 5 genomic contig, reference assembly	50.0 131 2%	0.014 100%
NT_009237.17	Homo sapiens chromosome 11 genomic contig, reference assembly	50.0 131 5%	0.014 92%
NT_007819.16	Homo sapiens chromosome 7 genomic contig, reference assembly	50.0 347 6%	0.014 96%
NT_010966.13	Homo sapiens chromosome 18 genomic contig, reference assembly	50.0 50.0 1%	0.014 87%
NT_010393.15	Homo sapiens chromosome 16 genomic contig, reference assembly	50.0 131 3%	0.014 92%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	50.0 176 3%	0.014 100%
NT_006713.14	Homo sapiens chromosome 5 genomic contig, reference assembly	50.0 135 1%	0.014 88%
NW_001838061.2	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188362)	46.4 251 1%	0.18 92%
NW_001838006.2	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on HuRef SCAF_1103279188397)	46.4 130 1%	0.18 93%
NW_001838988.2	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279187031)	46.4 46.4 1%	0.18 93%
NT_025741.14	Homo sapiens chromosome 6 genomic contig, reference assembly		0.18 93%
NT_113898.1	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4 46.4 1%	0.18 88%
NT_007302.13	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4 46.4 1%	0.18 88%
NT_030059.12	Homo sapiens chromosome 10 genomic contig, reference assembly	46.4 171 1%	0.18 93%
NW_001838769.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188433)	44.6 210 4%	0.62 96%
NW_001838115.2	Homo sapiens chromosome 14 genomic contig, alternate assembly (based on HuRef SCAF_1103279188327)	44.6 85.5 2%	0.62 96%
NW_001838461.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on HuRef SCAF_1103279188344)	44.6 44.6 1%	0.62 90%
NW_001838768.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188306)	44.6 44.6 1%	0.62 83%
NW_001838987.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188274B)	44.6 85.5 1%	0.62 92%
NW_001838928.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188369)		
NW_001838915.1	alternate assembly (based on HuRef SCAF_1103279188399)	44.6 249 1%	0.62 96%
NW_001838878.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188187)	44.6 85.5 1%	0.62 90%
NW_001838953.2	alternate assembly (based on HuRef SCAF_1103279188146)		
NT_026437.11	Homo sapiens chromosome 14 genomic contig, reference assembly	44.6 249 2%	0.62 92%
NT_016354.18		44.6 536 1%	0.62 96%

	Homo sapiens chromosome 4 genomic contig, reference assembly		•••••			
NT_023935.17	Homo sapiens chromosome 9 genomic contig, reference assembly	44.6	130	3%	0.62	92%
NT_008470.18	Homo sapiens chromosome 9 genomic contig, reference assembly	44.6	169	4%	0.62	93%
NT_022459.14	Homo sapiens chromosome 3 genomic contig, reference assembly	44.6	85.5	1%	0.62	90%
NT_032977.8	Homo sapiens chromosome 1 genomic contig, reference assembly	44.6	374	3%	0.62	96%
NT_010859.14	Homo sapiens chromosome 18 genomic contig, reference assembly	44.6	44.6	1%	0.62	90%

Alignments

```
>ref|NM 003107.2| Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA
Length=4912
GENE ID: 6659 SOX4 | SRY (sex determining region Y)-box 4 [Homo sapiens]
(Over 10 PubMed links)
Score = 5012 bits (5558), Expect = 0.0 Identities = 2789/2793 (99%), Gaps = 2/2793 (0%)
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Sbjct Query	2249 1865	ttaaagagaaaaagggaaaaaagaaagaaaagtaagcagggCTCG-TTCGCCCGCGTTCT	2308 1923
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         GCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCCAGA
                                                      2702
Query
         Sbjct
     3089
         GCGGCTGCTGGGCCTCCGCCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCCAGA
                                                      3148
     2703
         2762
Query
         Sbjct
     3149
                                                      3208
         Query
     2763
                                  2795
         Sbjct
     3209
         CGAGTGGTTTCGGAAAAAAAAAAAAAAAAAAAAAAA
>ref|NM_003108.3| Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA
Length=8737
GENE ID: 6664 SOX11 | SRY (sex determining region Y)-box 11 [Homo sapiens] (Over 10 PubMed links)
                                         Sort alignments for this subject seq
                                           E value Score Percent identity
                                           Query start position Subject star
Score = 309 bits (342), Expect = 1e-80 Identities = 224/259 (86%), Gaps = 0/259 (0%)
Strand=Plus/Plus
Query
     491
        CGACCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCAT
                                                      550
                             CGACCCAGACTGGTGCAAGACGGCGTCGGGCCACATCAAGCGGCCGATGAACGCGTTCAT
Sbjct
     166
                                                      225
Query
     551
        GGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCGACATGCACAACGC
                                                      610
        226
                                                      285
Sbjct
        CGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC
                                                      670
     611
Query
     286
        ĊĠŔĠŔŦĊŦĊĊŔŔĠŔĠĠĊŦĠĠĠĊŔŔĠĊĠĊŦĠĠŔŔĸĸŦĠĊŦĠŔŔĠĠŔĊŔĠĊĠŔĠŔŔŔĠŔŦĊĊĊ
Sbjct
                                                      345
     671
        TTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAA
                                                      730
Query
         GTTCATCCGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCCGACTACCCCGACTACAA
Sbjct
     346
                                                      405
        GTACCGGCCCAGGAAGAAG
                        749
Query
     731
        GTACCGGCCCCGGAAAAAG
Sbjct
     406
                        424
```

Score = 131 bits (144), Expect = 5e-27 Identities = 96/112 (85%), Gaps = 0/112 (0%)

```
NCBI Blast:X70683:H.sapiens mRNA for SOX-4 protein
   Strand=Plus/Plus
  Query
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             GGCTCCCACTTCGAGTTCCCCGACTACTGCACGCCGGAGCTGAGCGAGATGATCGCGGGG
  Sbjct
        1277
                                                                 1336
        1731
             GACTGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGAAGGGCGC
  Query
             GACTGGCTGGAGGCGAACTTCTCCGACCTGGTGTTCACATATTGAAAGGCGC
        1337
                                                          1388
  Sbjct
  >ref|NM_006943.2| Homo sapiens SRY (sex determining region Y)-box 12 (SOX12), mRNA
  Length=4645
  GENE ID: 6666 SOX12 | SRY (sex determining region Y)-box 12 [Homo sapiens] (10 or fewer PubMed links)
                                                  Sort alignments for this subject seq
                                                    E value Score Percent identity
                                                    Query start position Subject star
   Score = 291 bits (322), Expect = 3e-75 Identities = 213/246 (86%), Gaps = 1/246 (0%)
   Strand=Plus/Plus
        494
            CCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCATGGT
                                                                553
  Query
            Sbjct
        418
                                                                476
            GTGGTCGCAGATCGAGCGCCCAAGATCATGGAGCAGTCGCCCGACATGCACACGCCGA
                                                                613
  Query
        554
            ĠŤĠĠŤĊĠĊĀĠĊAĊĠĀAĊĠĠĊĠĠĀĀĠĀŤĊĀŤĠĠĀĊĊĠĠŤĠĠĊĊĊĠĀĊĀŤĠĊĀĊĀĊĠĊĊĠĀ
  Sbjct
        477
                                                                536
        614
            GATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT
                                                                673
  Query
                              ĠĂŤĊŤĊĊĂĂĠĊĠĊĊŤĠĠĠĊĊĠĊĆĠĊŤĠĠĊĂĠĊŤĠĊŤĠĊĂĠĠĂĊŦĊĠĠĂĠĂĂĠĂŤĊĊĊĠŤŤ
        537
                                                                596
  Sbjct
  Query
        674
            CATTCGAGAGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA
                                                                733
            597
                                                                656
  Sbjct
            CCGGCC
                   739
  Query
        734
             657
            CCGGCC
                   662
  Sbjct
   Score = 131 bits (144), Expect = 5e-27
   Identities = 90/102 (88%), Gaps = 0/102 (0%)
   Strand=Plus/Plus
        1674
             {\tt TCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGAGAC}
                                                                 1733
  Query
             1177
                                                                 1236
  Sbjct
        1734
             TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGA 1775
  Query
                    TGGCGCCCGTCTAGCATCGCAGACCTGGTTTTCACCTACTGA
  Sbjct
  >ref|NM_006941.3| Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA
  Length=2882
  GENE ID: 6663 SOX10 | SRY (sex determining region Y)-box 10 [Homo sapiens] (Over 10 PubMed links)
   Score = 167 bits (184), Expect = 7e-38 Identities = 173/224 (77%), Gaps = 2/224 (0%)
   Strand=Plus/Plus
            GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT
                                                                580
  Query
            Sbjct
        584
                                                                643
        581
            CATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG
                                                                640
  Query
```

GAAGCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCC

644

641

Sbjct

Query

703

699

```
GAGGCTGCTGAACGAAAGTGACAAGCGCCCCTTCA-TCGAGGAGGCTGAGCGGCTCCGTA
Sbict
Query
      700
          TCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG
          763
                                                  806
Sbjct
>ref|NM_000346.2| Homo sapiens SRY (sex determining region Y)-box 9 (campomelic
dysplasia, autosomal sex-reversal) (SOX9), mRNA Length=3935
GENE ID: 6662 SOX9 | SRY (sex determining region Y)-box 9 (campomelic
dysplasia, autosomal sex-reversal) [Homo sapiens] (Over 10 PubMed links)
Score = 156 bits (172), Expect = 1e-34 Identities = 166/219 (75%), Gaps = 0/219 (0%)
Strand=Plus/Plus
          GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT
Query
      521
                                                                580
          Sbjct
      681
                                                                740
          CATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG
Query
      581
                                                                640
          741
                                                                800
Sbjct
Query
      641
          GAAGCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCT
                                                                700
             GAGACTTCTGAACGAGAGCGAGAAGCGGCCCTTCGTGGAGGAGGCGGAGCGGCTGCGCGT
Sbjct
      801
                                                                860
      701
          CAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
Query
          899
Sbjct
      861
>ref|NM_007084.2| Homo sapiens SRY (sex determining region Y)-box 21 (SOX21), mRNA
Length=2537
GENE ID: 11166 SOX21 | SRY (sex determining region Y)-box 21 [Homo sapiens]
(10 or fewer PubMed links)
Score = 140 bits (154), Expect = 1e-29 Identities = 164/219 (74%), Gaps = 2/219 (0%)
Strand=Plus/Plus
      522 CACATCAAGCGACCCATGAACGCCTTCATGGTGGTCGCAGATCGAGCGGCGCAAGATC
                                                                581
Query
          CACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGTCGCGGGCTCAGCGGCGCAAGATG
      105
                                                                164
Sbjct
          \tt ATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGG
                                                                641
      582
Query
                    GCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCTTGGGCGCCGAGTGG
Sbjct
      165
                                                                224
                                                                700
Ouerv
      642
          AAGCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCT
          225
                                                                283
Sbjct
      701
Query
          CAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
                                              739
          322
Sbjct
      284
>ref|NM_006942.1| Homo sapiens SRY (sex determining region Y)-box 15 (SOX15), mRNA
Length=1394
GENE ID: 6665 SOX15 | SRY (sex determining region Y)-box 15 [Homo sapiens] (Over 10 PubMed links)
Score = 129 bits (142), Expect = 2e-26 Identities = 158/213 (74%), Gaps = 2/213 (0%)
Strand=Plus/Plus
          AAGCGACCCATGAACGCCTTCATGGTGTGGT-CGCAGATCGAGCGGCGCAAGATCATGGA
                                                                586
      528
Query
          AAGCGGCCGATGAACGCGTTCATGGTGTGGAGCTCCGCTC-AGCGCCGCCAGATGGCGCA
      642
                                                                700
Sbjct
Query
      587
          GCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCT
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```
GCAGAACCCCAAGATGCACAACTCCGAGATCTCCAAGCGCCTGGGCGCGCAGTGGAAGCT
Sbict
          GCTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA
Query
      647
                                                                706
                   761
          ĠĊŢĠĠĂĊĠĂĠĠĀĊĠĂĠĂĠĊĠĠĊĊĊŢŢĊĠŢĠĠĠĠĠĠĠĊĊĸĂĠĊĠĠĊŢĊĊĠĊĠĊĊĊĠĀĊĀ
                                                                820
Sbjct
      707
          CATGGCTGACTACCCCGACTACAAGTACCGGCC
                                        739
Query
                CCTGCGCGACTACCCGGCC
      821
Sbjct
>ref|NM_014587.2| Homo sapiens SRY (sex determining region Y)-box 8 (SOX8), mRNA
Length=3069
GENE ID: 30812 SOX8 | SRY (sex determining region Y)-box 8 [Homo sapiens]
(Over 10 PubMed links)
Score = 127 bits (140), Expect = 7e-26
Identities = 179/252 (71%), Gaps = 6/252 (2%)
Strand=Plus/Plus
          \verb|AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAG|
      528
                                                                587
Query
          Sbjct
          481
      588
          CAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTG
                                                                647
Query
          482
Sbjct
                                                                541
      648
          CTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCAC
                                                                707
Query
               ĊŤĠĂĠĊĠĂĠĂĠĊĠĂĠĂĠĊĠĠĊĆĊŤŤĊĠŤĠĠĄĠĠĠĊŔĠĂĠĊĠĊĊŤŤĊĠĊĠŤĠĊĂĠĊŔĊ
Sbjct
      542
                                                                601
          ATGGCTGACTACCCCGACTACAAGTAC----CGGCCCAGGAAGAAGGTGAAGTCCGGC
                                                                761
Query
          AAGAAGGACCÁCCCGÁCTÁCÁAGTÁCCAGCCACGCACGAAAGACCCAAAGCCGGC
                                                                661
Sbjct
Query
      762
          AACGCCAACTCC
                      773
               662
          CACAGCGACTCC
                      673
Sbjct
>ref|NM_031439.2| Homo sapiens SRY (sex determining region Y)-box 7 (SOX7), mRNA
Length=3219
GENE ID: 83595 SOX7 | SRY (sex determining region Y)-box 7 [Homo sapiens]
(10 or fewer PubMed links)
Score = 113 bits (124), Expect = 1e-21 Identities = 159/223 (71%), Gaps = 3/223 (1%)
Strand=Plus/Plus
      530
         GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCA
                                                                589
Query
          ĠĊĠĠĊĊĊĂŢĠĂĂĊĠĊĊŢŢĊĂŢĠĠŢŢŢĠĠĠĊĊĀĀĠĠĀĠĀĠĠĀĀAĊĠĠĊŢĠĠĊĀĠŢĠĊĀ
      217
                                                                276
Sbjct
      590
          GTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCT
                                                                649
Query
                GAACCCGGÁCCTGCÁCÁACGCCGÁGCTCAGCÁAGATGCTGGGAÁGTCGTGGÁÁGGCGCT
Sbjct
          CAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACAT
                                                                709
Query
          337
                                                                396
Sbjct
      710
          GGCTGACTACCCCGACTACAAGTACCGGCC---CAGGAAGAAG
                                                 749
Query
              GCAGGACTACCCCAACTACAAGTACCGGCCGCGCAGGAAGAAG
Sbjct
      397
                                                 439
>ref|NM_018419.2| Homo sapiens SRY (sex determining region Y)-box 18 (SOX18), mRNA
Length=1718
GENE ID: 54345 SOX18 | SRY (sex determining region Y)-box 18 [Homo sapiens] (Over 10 PubMed links)
Score = 107 bits (118), Expect = 6e-20 Identities = 160/223 (71%), Gaps = 8/223 (3%)
Strand=Plus/Plus
```

```
580
      521
          GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT
Query
          359
                                                                  415
Sbjct
          CATGG---AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACG
      581
                                                                  637
Query
          GCTGGCTCAGCAGAACCCGGACCTGCACAACGCGGTGCTCAGCAAGATGCTGGGCAAAGC
      416
                                                                  475
Sbjct
          CTGGAAGCTGCTCAAAGACAGCG-ACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGC
Query
      638
                                                                  696
                 GTGGAAGGAGCTGAACG-CGGCGGAGAAGCGGCCCTTCGTGGAGGAAGCCGAACGGCTGC
      476
                                                                  534
Sbjct
Query
      697
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                GCGTGCAGCACTTGCGCGACCACCCCAACTACAAGTACCGGCC
Sbjct
      535
>ref|NM_004189.2| Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA
Length=818
 GENE ID: 8403 SOX14 | SRY (sex determining region Y)-box 14 [Homo sapiens]
(10 or fewer PubMed links)
Score = 104 bits (114), Expect = 8e-19 Identities = 161/224 (71%), Gaps = 12/224 (5%)
 Strand=Plus/Plus
      522
          CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
                                                                  581
Query
          CÁCATCAAGCGGCCCATGAACGCCTTCATGGTATGGTCCCGGGGCCAGCGGCGCAAGATG
                                                                  126
Sbjct
      582
          ATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG---CAAACGC
                                                                  638
Query
                     GCCCAGGAAAACCCCAAGATGCACAACTCGGAGATCAGCAAACGCCTAGGTGCCGAA---
Sbjct
      127
                                                                  183
          TGGAAGCTGC--TCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTG
      639
                                                                  695
Query
          184
                                                                 240
Sbjct
          \tt CGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
      696
Query
                          241
          CGCGCCCAGCACATGAAGGAGCACCCTGACTACAAGTACCGACC
                                                   284
Sbjct
>ref|NM_022454.3| Homo sapiens SRY (sex determining region Y)-box 17 (SOX17), mRNA
Length=2350
GENE ID: 64321 SOX17 | SRY (sex determining region Y)-box 17 [Homo sapiens] (10 or fewer PubMed links)
Score = 100 bits (110), Expect = 9e-18 Identities = 153/214 (71%), Gaps = 8/214 (3%)
 Strand=Plus/Plus
          GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGCGCAAGATCATGGAGCA
                                                                  589
Query
          GCGGCCGATGAACGCTTTCATGGTGTGGGCTAAGGACGAGCG---CAAGCGGCTGGCGCA
      411
Sbjct
                                                                  467
          {\tt GTCG---CCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCT}
      590
                                                                  646
Query
               GCAGAATCCAGACCTGCACAACGCCGAGTTGAGCAAGATGCTGGGCAAGTCGTGGAAGGC
Sbjct
      468
                                                                  527
      647
          GCTCAAAGACAGCG-ACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGC
                                                                  705
Query
                                         GCTGAC-GCTGGCGGAGAAGCGGCCCTTCGTGGAGGAGGCAGAGCGGCTGCGCGTGCAGC
      528
                                                                  586
Sbjct
      706
          ACATGGCTGACTACCCCGACTACAAGTACCGGCC
                                          739
Query
          587
Sbjct
>ref|NM_005634.2| Homo sapiens SRY (sex determining region Y)-box 3 (SOX3), mRNA
Length=2074
GENE ID: 6658 \text{ SOX3} \mid \text{SRY (sex determining region Y)-box 3 [Homo sapiens]} (Over 10 PubMed links)
```

```
Score = 100 \text{ bits } (110),
                      Expect = 9e-18
Identities = 154/216 (71%), Gaps = 8/216 (3%)
Strand=Plus/Plus
                                                              584
Query
     528
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          477
Sbjct
      418
     585
          GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAG
                                                              644
Query
                 Sbjct
      478
          GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCCGCCGACTGGAAA
                                                              534
          CTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAA
                                                              703
Query
                             ĊŢĠĊŢĠĂĊĠĠĊĠĠĠĠĠĠĠĠĠĊĊĂŢŢĊĂŢĊĠĠĠĠĠĠĊĊĀĠĠĠĠĊŢŢĊĠĊĠĊĠŢ
     535
                                                              593
Sbjct
     704
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                                          739
Query
                  Sbjct
     594
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                                          629
>ref|NM_005986.2| Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), mRNA
Length=4108
GENE ID: 6656 SOX1 | SRY (sex determining region Y)-box 1 [Homo sapiens]
(10 or fewer PubMed links)
Score = 96.9 bits (106), Expect = 1e-16
Identities = 152/215 (70%), Gaps = 2/215 (0%)
Strand=Plus/Plus
     526
          {\tt TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGCGCAAGATCATGG}
                                                              585
Query
          212
Sbjct
          AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGC
Query
     586
          AGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCGAGTGGAAGG
Sbjct
     272
                                                              331
          {\tt TGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAAG}
                                                              704
Query
     646
                             TCATGTCCGAGGCCGAGAAGCGGCCGTTCA-TCGACGAGGCCAAGCGGCTGCGCGCGCTG
Sbjct
     332
                                                              390
          CACATGGCTGACTACCCCGACTACAAGTACCGGCC
     705
Query
                    CACATGAAGGAGCACCCGGATTACAAGTACCGGCC
Sbjct
>ref|NM_003106.2| Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA
Length=2518
GENE ID: 6657 SOX2 | SRY (sex determining region Y)-box 2 [Homo sapiens]
(Over 10 PubMed links)
Score = 91.5 bits (100), Expect = 5e-15 Identities = 153/219 (69%), Gaps = 2/219 (0%)
Strand=Plus/Plus
     526
          TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG
                                                              585
Ouerv
          549
                                                              608
Sbjct
Query
     586
          AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGC
                                                              645
                609
          AGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAAC
                                                              668
Sbjct
Query
     646
          TGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAAG
                                                              704
                     ŤTTŤGTCGĠÁGÁCGĠÁGÁĠĆGGĆĆGŤŤĊÁ–ŤĊĠÁCĠÁĠĠĆTAÁĠĆĠĠĆŤĠĆĠAGCGCTĠ
     669
Sbjct
     705
          CACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG
Query
                                            743
                    CACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGG
Sbjct
      728
>ref|NM 005686.2| Homo sapiens SRY (sex determining region Y)-box 13 (SOX13), mRNA
Length=4088
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GENE ID: 9580 SOX13 | SRY (sex determining region Y)-box 13 [Homo sapiens]

http://blast.ncbi.nlm.nih.gov/Blast.cgi

```
(Over 10 PubMed links)
Score = 78.8 bits (86), Expect = 3e-11 Identities = 153/218 (70%), Gaps = 10/218 (4%)
Strand=Plus/Plus
     522
            CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
                                                                     581
Query
           1862
                                                                     1921
Sbjct
      582
            ATG-GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG
                                                                     640
Query
                CTGCAAGCCTTC-CCAGACATGCACAACTCCAGCATCAGCAAGATCCTTGGATCTCGCTG
Sbjct
      1922
                                                                     1980
      641
            GAAG---CTGCTCAAAGACAGCGACAAG-ATCCCTTTCATTCGAGAGGCGGAGCGGCTGC
                                                                     696
Query
            1981
Sbjct
      697
            GCCTCAAGCACATGGCTGACTACCCCGACTACAAGTAC
Query
                 GCCGGCAGCACCTGGAGAAGTATCCTGACTACAAGTAC
Sbjct
      2037
                                                2074
>ref|XM_001713691.1| PREDICTED: Homo sapiens hypothetical protein LOC100130809 (LOC10013
mRNA
Length=897
Score = 64.4 bits (70), Expect = 7e-07 Identities = 94/126 (74%), Gaps = 8/126 (6%)
 Strand=Plus/Plus
      528
          AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCGCAAGAT---CAT
                                                                    583
Query
           AAGCGACCCATGAACGCATTCATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT
      329
                                                                    387
Sbjct
      584
          GGAGCAGTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA
Query
            AĞÂĞ-ÂATC-CCAĞÂ-ÂTĞCGAÂACTCAĞÂĞÂTCAĞCÂAĞCAĞCTĞĞĞATACCAĞTĞĞÂA
      388
Sbjct
          GCTGCT
      644
Query
             | | | | |
Sbjct
      445
          AATGCT
                  450
>ref|NM_003140.1| Homo sapiens sex determining region Y (SRY), mRNA
Length=897
 GENE ID: 6736 SRY | sex determining region Y [Homo sapiens]
(Over 10 PubMed links)
Score = 64.4 bits (70), Expect = 7e-07 Identities = 94/126 (74%), Gaps = 8/126 (6%)
Strand=Plus/Plus
           AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCGCAAGAT---CAT
                                                                    583
Query
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      584
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      644
           GCTGCT
                 649
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             | \cdot | \cdot |
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Sbjct
>ref|NM_152989.2| Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcri
variant 2, mRNA
Length=4563
GENE ID: 6660 \text{ SOX5} \mid \text{SRY (sex determining region Y)} - \text{box 5 [Homo sapiens]} (Over 10 PubMed links)
 Score = 57.2 bits (62), Expect = 1e-04
 Identities = 76/103 (73%), Gaps = 2/103 (1%)
 Strand=Plus/Plus
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           1995
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Ouerv
                       2054
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variant 1, mRNA
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(Over 10 PubMed links)
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 Identities = 76/103 (73%), Gaps = 2/103 (1%)
 Strand=Plus/Plus
      522
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Sbict
      581
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Sbjct 1824
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 GENE ID: 6660 SOX5 | SRY (sex determining region Y)-box 5 [Homo sapiens]
(Over 10 PubMed links)
Score = 57.2 bits (62), Expect = 1e-04 Identities = 76/103 (73%), Gaps = 2/103 (1%)
 Strand=Plus/Plus
      522
          CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT
Query
           ĊĂĊĂŤĂĂĂĠĊĠŦĊĊĂĂŤĠĂĂŤĠĊĊŤŤĊĂŤĠĠŤĠŤĠĠĠĊŦĂĂĂĠĂŤ–ĠĂĂĊĠĠĀĠĂĂĀĠĂŤ
      527
Sbjct
      581
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Query
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Sbjct
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Length=4556
 GENE ID: 112939 BTBD14B | BTB (POZ) domain containing 14B [Homo sapiens]
(10 or fewer PubMed links)
Score = 51.8 bits (56), Expect = 0.004 Identities = 34/38 (89%), Gaps = 0/38 (0%)
 Strand=Plus/Minus
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>ref|NM_033326.2| Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), transcri
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(Over 10 PubMed links)
Score = 50.0 bits (54), Expect = 0.014 Identities = 65/90 (72%), Gaps = 0/90 (0%)
 Strand=Plus/Plus
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       1859
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                                            611
Query
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(Over 10 PubMed links)
 Score = 50.0 bits (54), Expect = 0.014 Identities = 65/90 (72%), Gaps = 0/90 (0%)
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mRNA
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 Strand=Plus/Minus
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homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 1, mRNA \,
Length=7762
 GENE ID: 4301 MLLT4 | myeloid/lymphoid or mixed-lineage leukemia (trithorax
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 Score = 46.4 bits (50), Expect = 0.18 Identities = 31/35 (88%), Gaps = 0/35 (0%)
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Sbjct
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homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 2, mRNA Length=7551
 GENE ID: 4301 MLLT4 | myeloid/lymphoid or mixed-lineage leukemia (trithorax
homolog, Drosophila); translocated to, 4 [Homo sapiens] (Over 10 PubMed links)
 Score = 46.4 bits (50), Expect = 0.18 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Minus
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homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 3, mRNA
Length=4981
GENE ID: 4301 MLLT4 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Homo sapiens] (Over 10 PubMed links)
 Score = 46.4 bits (50), Expect = 0.18 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Minus
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                                         1189
Query
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                                         4
Sbjct
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>ref|NM_015156.2|
Length=5537
GENE ID: 23186 RCOR1 | REST corepressor 1 [Homo sapiens] (Over 10 PubMed links)
 Score = 44.6 bits (48),
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 Identities = 35/42 (83%), Gaps = 0/42 (0%)
 Strand=Plus/Plus
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           CGCCTCGGGCGCCGCCGCCTCCTCAGCCTCGGCCGCCGCCGC
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>ref|NT 007592.14|Hs6 7749 WHOMO sapiens chromosome 6 genomic contig, reference assembly
Length=48945890
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                                                E value Score Percent identity
                                                Query start position Subject star
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     12452671
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Query
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              12452790
Query
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              12452910
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     12452911
                                                                 12452970
     305
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Query
                                                                 364
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                                                                 12453150
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Query	665	GATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGA	724
Sbjct	12453331	GATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGA	12453390
Query	725 12453391	CTACAAGTACCGGCCCAGGAAGAAGGTGAAGTCCGGCCAACGCCAACTCCAGCTCCTCGGC	784 12453450
Sbjct Query	785	CGCCGCCTCCTCCAAGCCGGGGGAGaagaagaagaagaagaagagagagagagagaga	844
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Sbjct	12453511		12453570
Query	905	tgggggggggCCAACTCCAAACCGGCGCAGAAAAAGAGCTGCGGCTCCAAAGTGGCGGG	964
Sbjct	12453571		12453630
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Sbjct	12453631		12453690
Query	1025	cggcggGAAAGCAGCGGCTgccgccgccgcctccttcgccgccgaacaggcgggggccgc	1084
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Query	1205 12453871	CAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCTACCTGTTCGGCGGCCTGGGCACGTC	1264 12453930
Query	12455671	GTCGTCGCCCGTGGGCGGCGTGGGCGCGGGGGCCGACCCCAGCGACCCCCTGGGCCTGTA	1324
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Query	1325	CGAGGAGGAGGCGCGGCTGCTogocogacgogccagootgagcggccgcagoagcgc	1384
Sbjct	12453991		12454050
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Sbjct	12454051		12454110
Query	1445	cgeegestegeeegeeegteeagegeeeTCGCACGCGteetesteggeetegteea	1504
Sbjct	12454111	CGCCGCCTCGCCCGTCCAGCGCGCCCTCGCACGCGTCCTCCTCGGCCTCGTCCCA	12454170
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Sbjct	12454171	CTCCTCCTCTCCTCCTCGGGCTCCTCGTCCTCCGACGACGAGTTCGAAGACGACCT	12454230
Query	1565	GCTCGACCTGAACCCCAGCTCAAACTTTGAGAGCATGTCCCTGGGCAGCTTCAGTTCGTC	1624
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Query	1625	GTCGGCGCTCGACCGGGACCTGGATTTTAACTTCGAGCCCGGCTCCGGCTCGCACTTCGA	1684
Sbjct Query	12454291 1685	GTCGGCGCTCGACCGGGACCTGGATTTTAACTTCGAGCCCGGCTCCGGCTCGCACTTCGA GTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCGAGTC	12454350 1744
Sbjct	12454351	GTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCGAGTC	12454410
	10 1001		

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butyrophilin, subfamily 2, member Al isoform 1 precursor butyrophilin, subfamily 2, member Al isoform 2 precursor
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Score = 41.0 bits (44), Expect = 7.5 Identities = 30/35 (85%), Gaps = 0/35 (0%) Strand=Plus/Plus

ACCTGTGATTGTTGTTGATGTTGTTGATG Query 2048

> Sort alignments for this subject seq E value Score Percent identity Query start position Subject star

Features in this part of subject sequence: SRY (sex determining region Y)-box 4

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Score = 1570 bits (1740), Expect = 0.0 Identities = 870/870 (100%), Gaps = 0/870 (0%) Strand=Plus/Plus
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Query	125	CTATAACTCCTCTGCGAGAGGCGGAGAACTCCTTCCCCAAATCTTTTGGGGACTTTTCTC	184
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Query	185	TCTTTACCCACCTCCGCCCTGCGAGGAGTTGAGGGGCCAGTTCGGCCGCGCGCG	244
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Query	425	CCTCGAGCTGGGAATCGCCTCCTCCCCCACGCCCGGCTCCACCGCCTCCACGGGCGGCAA	484
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Query	485	GGCCGACGACCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGC	544
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CBI Blas	t:X70683:H.	sapiens mRNA for SOX-4 protein	Page 23
Query	725	CTACAAGTACCGGCCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGC	784
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		s part of subject sequence: rmining region Y)-box 4	
Ident		ts (1648), Expect = 0.0 9/831 (99%), Gaps = 1/831 (0%) s	
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Sbjct -	17885427	GGGGCGGAGGACACGAACTGGAAGGGGGTTCACGGTCAAACTGAAATGGATTTGCAC	17885486
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Query	2685	GAGGTGAGACTTCCCAGACCCCGGAGGCGTGGAGGAGAGAGA	2744
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17885607

2745

Query

Sbjct

17885657

>ref|NW_001838765.1|Hs2_WGA158_36 Momo sapiens chromosome 2 genomic contig, alternate asse (based on HuRef SCAF_1103279188139) Length=2797789

Sort alignments for this subject seq E value Score Percent identity Query start position Subject star

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Score = 309 bits (342), Expect = 1e-80 Identities = 224/259 (86%), Gaps = 0/259 (0%)
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            719581
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Sbjct
     551
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                                                               610
Query
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     719641
                                                               719700
Sbjct
            CGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC
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                                                               670
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                                                               719760
Sbjct
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     671
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                                                               730
            Sbjct
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                                                               719820
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Sbjct
Features in this part of subject sequence:
  SRY-box 11
Score = 131 bits (144), Expect = 5e-27 Identities = 96/112 (85%), Gaps = 0/112 (0%)
Strand=Plus/Plus
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                                                               720751
Sbjct
     1731
            {\tt GACTGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGAAGGGCGC}
Query
                                                       1782
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Sbjct
>ref|NT_005334.15|Hs2_5491 Weak Homo sapiens chromosome 2 genomic contig, reference assembly
Length=11088087
                                              Sort alignments for this subject seq
                                                E value Score Percent identity
                                                Query start position Subject star
Features in this part of subject sequence:
  SRY-box 11
Score = 309 bits (342), Expect = 1e-80 Identities = 224/259 (86%), Gaps = 0/259 (0%)
Strand=Plus/Plus
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                                                               550
Query
            Sbjct
     667099
                                                               667158
Query
     551
            GGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCGACATGCACACGC
                                                               610
            GGTATGGTCCAAGATCGAACGCAGGAAGATCATGGAGCAGTCTCCGGACATGCACAACGC
     667159
                                                               667218
Sbjct
     611
            CGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC
                                                               670
Query
            667219
                                                               667278
Sbjct
Query
     671
            TTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAA
                                                               730
             GTTCÁTCCGGGÁGCGGÁGCGGCTGCGGCTCÁAGCÁCATGGCCGÁCTÁCCCCGÁCTÁCÁA
     667279
                                                               667338
```

731

GTACCGGCCCAGGAAGAAG 749

Sbjct

Query

```
GTACCGGCCCCGGAAAAAG
     667339
Sbjct
                                 667357
Features in this part of subject sequence:
  SRY-box 11
Score = 131 bits (144), Expect = 5e-27 Identities = 96/112 (85%), Gaps = 0/112 (0%)
 Strand=Plus/Plus
Query 1671
             GGCTCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGA
                                                                      1730
             GGCTCCCACTTCGAGTTCCCCGACTACTGCACGCCGGAGCTGAGCGAGATGATCGCGGGG
      668210
                                                                       668269
Sbjct
      1731
             GACTGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGAAGGGCGC
                                                               1782
Query
              Sbjct
      668270
             GACTGGCTGGAGGCGAACTTCTCCGACCTGGTGTTCACATATTGAAAGGCGC
                                                                668321
>ref|NW_001838652.1|Hs20_WGA1211_36 Dominion of the sapiens chromosome 20 genomic contig, alternate a
(based on HuRef SCAF_1103279188366)
Length=22415471
                                                    Sort alignments for this subject seq
                                                      E value Score Percent identity
                                                      Query start position Subject star
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 12
 Score = 291 bits (322), Expect = 3e-75 Identities = 213/246 (86%), Gaps = 1/246 (0%)
 Strand=Plus/Plus
Query 494
             \verb|CCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCATGGT|\\
                                                                       553
             258081
                                                                       258139
Sbjct
              GTGGTCGCAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCCGACATGCACACGCCGA
      554
Query
                        GTGGTCGCAGCACGAACGCCGAAGATCATGGACCAGTGGCCCGACATGCACAACGCCGA
      258140
                                                                       258199
Sbjct
             GATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT
Query
      614
                                                                       673
             258200
                                                                       258259
Sbjct
Query
      674
             CATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA
                                                                       733
               CGTGCGGGAGGCGGCTGCGGCTCAAGCACATGGCGGATTACCCGGACTACAAGTA
      258260
                                                                       258319
Sbjct
      734
              CCGGCC
                     739
Query
              258320
             CCGGCC
                     258325
Sbjct
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 12
 Score = 131 bits (144), Expect = 5e-27
 Identities = 90/102 (88%), Gaps = 0/102 (0%)
Strand=Plus/Plus
             TCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGAGAC
Query 1674
                                                                       1733
              ŤĊĠĊŔĊŤŤĊĠŔĠŤŤĊĊĊĠĠŔĊŤŔĊŤĠĊŔĊĊĊĊĠŔĠĠŤŦŔĊĊĠŔĠŔŤĠŔŤĊĠĊĠĠĠĠĠŔĊ
Sbjct
      258840
                                                                       258899
      1734
              TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGA
Query
                    TGGCGCCCGTCTAGCATCGCAGACCTGGTTTTCACCTACTGA
                                                      258941
Sbjct
      258900
Features in this part of subject sequence:
  similar to hCG2045825
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus
```

```
CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
Query 1148
                                                   1186
                    CĠĊĊŤĊĊĠĊĊŤĊĊĠĊĊŤĊĊĠĊĊŤĊĊĠĊĊŤĊĊĠĊ
      9967415
                                                   9967377
Sbjct
Features in this part of subject sequence: similar to hCG2045825
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Minus
              CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
Query 1148
                                                   1186
              CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC
Sbjct 9967421
                                                   9967383
Features in this part of subject sequence:
  similar to hCG2045825
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus
Query 1148
              CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
              9967427
              CGCCTCCGCCTCCGCCTCCGCCTCCGC
                                                   9967389
Features in this part of subject sequence:
  similar to hCG2045825
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Minus
Query 1148
              CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
                                                   1186
              Sbjct 9967433
>ref|NT_011387.8|Hs20_11544 Memo sapiens chromosome 20 genomic contig, reference assembly
Length=26259569
                                                   Sort alignments for this subject seq
                                                     E value Score Percent identity
                                                     Query start position Subject star
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 12
Score = 291 bits (322), Expect = 3e-75 Identities = 213/246 (86%), Gaps = 1/246 (0%)
 Strand=Plus/Plus
Query 494
             CCCGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCTTCATGGT
             Sbjct
      246656
                                                                     246714
             GTGGTCGCAGATCGAGCGCCCAAGATCATGGAGCAGTCGCCCGACATGCACAACGCCGA
Query
      554
                                                                     613
             ĠŢĠĠŢĊĠĊĄĠĊĄĊĠĄĄĊĠĠĊĠĠĄĄĠĄŢĊĄŢĠĠĄĊĊĠĠĊĊĠĄĊĄŢĠĊŔĊĄĊĠĊĠĄ
      246715
                                                                     246774
Sbjct
      614
             GATCTCCAAGCGGCTGGGCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT
Query
             246775
                                                                     246834
Sbjct
Query
      674
             CATTCGAGAGGCGGAGCGCCTCCAAGCACATGGCTGACTACCCCGACTACAAGTA
                                                                     733
             246835
Sbjct
      734
             CCGGCC
                    739
Query
             CCGGCC
Sbjct
      246895
                    246900
```

Features in this part of subject sequence:

```
SRY (sex determining region Y)-box 12
 Score = 131 bits (144), Expect = 5e-27 Identities = 90/102 (88%), Gaps = 0/102 (0%)
 Strand=Plus/Plus
Query 1674
               TCGCACTTCGAGTTCCCGGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGAGAC
              247415
Sbjct
      1734
              \tt TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGA
                                                         1775
Query
                     Sbjct 247475 TGGCGCCCGTCTAGCATCGCAGACCTGGTTTTCACCTACTGA
Features in this part of subject sequence:
  similar to hCG2045825
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus
Query 1148
               CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
     9955587 CGCCTCCGCCTCCGCCTCCGCCTCCGC
Sbjct
                                                        9955549
Features in this part of subject sequence: similar to hCG2045825 \,
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84\%), Gaps = 0/39 (0\%)
Strand=Plus/Minus
Query 1148
                CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
                1 11111 1111111
Sbjct 9955593
               CGCCTCCGCCTCCGCCTCCGCCTCCGC
                                                        9955555
Features in this part of subject sequence:
  similar to hCG2045825
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Minus
               CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
Query 1148
                                                        1186
                1 11111 1111111
               CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC
Sbict 9955599
                                                        9955561
Features in this part of subject sequence:
  similar to hCG2045825
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus
Query 1148
               CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
                                                        1186
                CGCCTCCGCCTCCGCCTCCGCCTCCGC
Sbjct 9955605
                                                        9955567
>ref|NW_001838084.2|Hs13_WGA793_36 Momo sapiens chromosome 13 genomic contig, alternate as
(based on HuRef SCAF_1103279188152)
Length=25468656
                                                        Sort alignments for this subject seq
                                                          E value Score Percent identity
                                                          Query start position Subject star
Features in this part of subject sequence:
  SRY-box 21
```

Score = 140 bits (154),

Expect = 1e-29

Identities = 164/219 (74%), Gaps = 2/219 (0%)

```
Strand=Plus/Plus
Query
     522
             CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
             16996200
             CÁCGTCÁÁGCGGCCCÁTGÁÁCGCCTTCÁTGGTGTGGTCGCGGGCTCÁGCGGCGCÁÁGÁTG
                                                                16996259
Sbjct
     582
             ATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGG
                                                                641
Query
                       GCCCAGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCTTGGGCGCCGAGTGG
     16996260
                                                                16996319
Sbjct
             AAGCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCT
Query
             16996320
                                                                16996378
Sbjct
             CAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
Query
     701
                                               739
             16996379
                                               16996417
Sbjct
Features in this part of subject sequence:
  hypothetical protein
Score = 42.8 bits (46), Expect = 2.2 Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Minus
Query 2050
            CTGTGATTGTTGTTGATGTTGTTGA
             1920740
            CTGTGGTTGTTGTTGTTGTTGA
                                       1920710
Sbjct
```

> Sort alignments for this subject seq E value Score Percent identity Query start position Subject star

Features in this part of subject sequence: SRY-box 21

```
Score = 140 bits (154), Expect = 1e-29 Identities = 164/219 (74%), Gaps = 2/219 (0%) Strand=Plus/Minus
```

```
522
            CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
                                                          581
Query
            CACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGTCGCGGGCTCAGCGGCGCAAGATG
Sbjct
     8453961
                                                          8453902
     582
            ATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGG
                                                          641
Query
            8453901
                                                          8453842
Sbjct
     642
            AAGCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCT
                                                          700
Query
                        8453841
           AAACTGCTCACAGAGTCGGAGAAGCGGCCGTTCAT-CGACGAGGCCAAGCGTCTACGCGC
Sbjct
                                                          8453783
            CAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
Query
     701
                                          739
            CATGCACATGAAGGAGCACCCCGACTACAAGTACCGGCC
     8453782
                                          8453744
Sbjct
```

Features in this part of subject sequence: insulin receptor substrate 2 hypothetical protein

```
Score = 42.8 bits (46), Expect = 2.2 Identities = 28/31 (90\%), Gaps = 0/31 (0\%) Strand=Plus/Plus
```

```
Features in this part of subject sequence:
  SRY-box 15
 Score = 129 bits (142), Expect = 2e-26 Identities = 158/213 (74%), Gaps = 2/213 (0%)
 Strand=Plus/Minus
              AAGCGACCCATGAACGCCTTCATGGTGTGGT-CGCAGATCGAGCGGCGCAAGATCATGGA
      528
Query
Sbjct
      7078179
              AAGCGGCCGATGAACGCGTTCATGGTGTGGAGCTCCGCTC-AGCGCCGCCAGATGGCGCA
                                                                     7078121
      587
              GCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCT
Query
              7078120
                                                                     7078061
Sbjct
      647
              GCTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA
                                                                     706
Query
                        GCTGGACGAGGACGAGAAGCGGCCCTTCGTGGAGGAGGCCAAGCGGCTCCGCGCCCGACA
      7078060
                                                                     7078001
Sbjct
      707
              CATGGCTGACTACCCGGACTACAAGTACCGGCC
Query
                    7078000
              CCTGCGCGACTACCCGGCC
                                             7077968
Sbjct
>ref|NT_010718.15|Hs17_10875 Memo sapiens chromosome 17 genomic contig, reference assembly
Length=21163833
Features in this part of subject sequence:
  SRY-box 15
Score = 129 bits (142), Expect = 2e-26 Identities = 158/213 (74%), Gaps = 2/213 (0%)
 Strand=Plus/Minus
      528
              AAGCGACCCATGAACGCCTTCATGGTGTGGT-CGCAGATCGAGCGGCGCAAGATCATGGA
Query
              AAGCGGCCGATGAACGCGTTCATGGTGTGGAGCTCCGCTC-AGCGCCGCCAGATGGCGCA
                                                                     7090137
Sbjct
      7090195
      587
              GCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGCT
                                                                     646
Query
                    GCAGAACCCCAAGATGCACAACTCCGAGATCTCCAAGCGCCTGGGCGCGCAGTGGAAGCT
                                                                     7090077
Sbjct
      7090136
      647
              GCTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA
                                                                     706
Query
              Sbjct
      7090076
                                                                     7090017
      707
              CATGGCTGACTACCCCGACTACAAGTACCGGCC
                                             739
Query
              7090016
                                             7089984
Sbjct
>ref|NW_001838454.2|Hs17_WGA1163_36 Memo sapiens chromosome 17 genomic contig, alternate a
(based on HuRef SCAF_1103279188168)
Length=12595466
                                                   Sort alignments for this subject seq
                                                    E value Score Percent identity
                                                    Query start position Subject star
Features in this part of subject sequence:
  transcription factor SOX9
Score = 104 bits (114), Expect = 8e-19 Identities = 96/122 (78%), Gaps = 0/122 (0%)
Strand=Plus/Minus
Query
     521
              GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT
                                                                     580
              5396434
                                                                     5396375
Sbjct
      581
              {\tt CATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG}
                                                                     640
Query
                         CGCGGACCAGTACCCGCACTTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAAGCTCTG
      5396374
                                                                     5396315
Sbjct
Query
      641
              GΑ
                 642
```

GΑ

5396313

5396314

Sbjct

```
Features in this part of subject sequence:
  transcription factor SOX9
 Score = 59.0 bits (64), Expect = 3e-05 Identities = 70/95 (73%), Gaps = 0/95 (0%)
 Strand=Plus/Minus
              CTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAG
      645
Query
                                               Sbjct
      5395414
                                                                       5395355
      705
              CACATGGCTGACTACCCCGACTACAAGTACCGGCC
Query
              5395354
                                                5395320
Sbjct
 Features in this part of subject sequence:
  regulator of G-protein signaling 9 isoform 2
  regulator of G-protein signaling 9 isoform 1
Score = 42.8 bits (46), Expect = 2.2 Identities = 28/31 (90%), Gaps = 0/31 (0%)
 Strand=Plus/Plus
               CTGTGATTGTTGTTGATGTTGTTGA
Query 2050
               CTGTTGTTGTTATTGCTGTTGTTGA
Sbjct 12330673
                                             12330703
 Features flanking this part of subject sequence:
  13946 bp at 5' side: voltage-dependent calcium channel gamma-5 subunit isoform b 59295 bp at 3' side: protein kinase C, alpha
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
               TGTGATTGTTGTTGATGTTGTTGATG
Query 2051
                                              2082
               10658531
Sbjct
>ref|NW_001838884.2|Hs3_WGA277_36 Momo sapiens chromosome 3 genomic contig, alternate asse
(based on HuRef SCAF_1103279188385)
Length=64955803
                                                   Sort alignments for this subject seq
                                                     E value Score Percent identity
                                                     Query start position Subject star
 Features in this part of subject sequence:
  SRY-box 14
 Score = 104 bits (114), Expect = 8e-19 Identities = 161/224 (71%), Gaps = 12/224 (5%)
 Strand=Plus/Minus
      522
               CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
Query
               56570705
Sbjct
      56570764
      582
               ATGGAGCAGTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGG---CAAACGC
                                                                       638
Query
               Sbjct
      56570704
                                                                       56570648
               TGGAAGCTGC--TCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTG
Query
      639
                                                                       695
               TGGAAGCTTCTGTCCGAGGCA--GAGAAGCGGCCATACA-TCGATGAAGCCAAGCGGCTA
      56570647
                                                                       56570591
Sbjct
               CGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
      696
Query
                              Sbjct
      56570590
               CGCGCCCAGCACATGAAGGAGCACCCTGACTACAAGTACCGACC
                                                         56570547
 Features in this part of subject sequence:
```

sex-determining region Y-box 2

```
Score = 91.5 bits (100), Expect = 5e-15 Identities = 153/219 (69%), Gaps = 2/219 (0%)
 Strand=Plus/Minus
       526
                  TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG
                                                                                   585
Query
                  1111111111111
                 TCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCC
Sbjct
       12593937
                                                                                   12593878
                 586
                                                                                   645
Ouerv
Sbjct
       12593877
                                                                                   12593818
       646
                  TGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAAG
                                                                                   704
Query
                 12593817
                                                                                  12593759
Sbjct
Query
       705
                 CACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG
                               CACATGAAGGAGCACCCGGATTATAAATACCGGCCCCGG
Sbjct 12593758
                                                            12593720
 Features flanking this part of subject sequence:
   368249 bp at 5' side: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 isofor... 1716439 bp at 3' side: hypothetical protein LOC205428
 Score = 46.4 bits (50), Expect = 0.18
 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Plus
Query 2228
                 CATCACCACCTTGGTTTTGTTTTATTTTGCTTCTT
                                                        2262
                  Sbjct 48631837 CATCATCACTTTGGTTATGTTTTATTTTGGTTCTT
                                                        48631871
Features flanking this part of subject sequence: 555396 bp at 5' side: similar to peptidylprolyl isomerase A-like 680809 bp at 3' side: butyrylcholinesterase precursor
 Score = 42.8 bits (46), Expect = 2.2
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Plus
Query 2055
                 ATTGTTGTTATTGATGTTGTTGATG
                  Sbjct 27830621 ATTGTTGTTGTTGTTGTTGTTGATG 27830648
Features flanking this part of subject sequence: 8911 bp at 5' side: sterile alpha motif domain containing 7 40774 bp at 3' side: leucine rich repeat containing 31
 Score = 41.0 bits (44), Expect = 7.5 Identities = 31/37 (83%), Gaps = 0/37 (0%)
 Strand=Plus/Plus
Query 2056
                                                          2092
                  TTGTTGTTATTGATGTTGTTGATGGCAAAAAAA
Sbjct 24430482 TTGTTGTTATTGTTGTTGTTGTTCTGAAAAATAA
                                                          24430518
 Features flanking this part of subject sequence:
   360070 bp at 5' side: similar to hCG2021878
1305561 bp at 3' side: hypothetical protein LOC131149
 Score = 41.0 bits (44), Expect = 7.5
 Identities = 33/40 (82%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query 180
                  TTCTCTTTTACCCACCTCCGCCCCTGCGAGGAGTTGAGG
                                                              219
                  Sbjct 31502884
                 TTCTCTCTTTACACCACTCAGCCGCTGCCAGGGGTTGAGG
>ref|NT_010641.15|Hs17_10798 Momo sapiens chromosome 17 genomic contig, reference assembly
Length=11472733
```

Sort alignments for this subject seq

Query start position Subject star

```
Features in this part of subject sequence:
  transcription factor SOX9
Score = 104 bits (114), Expect = 8e-19
Identities = 96/122 (78%), Gaps = 0/122 (0%)
Strand=Plus/Plus
Query
      521
              GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT
             4044113
                                                                    4044172
Sbjct
              CATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG
Query
      581
                                                                    640
             4044173
                                                                    4044232
Sbjct
      641
              GA
                 642
Query
      4044233
                 4044234
Sbjct
             GΑ
Features in this part of subject sequence:
  transcription factor SOX9
Score = 59.0 bits (64), Expect = 3e-05 Identities = 70/95 (73%), Gaps = 0/95 (0%)
Strand=Plus/Plus
              \verb|CTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAG| \\
Query 645
                                                                    704
             Sbjct
      4045133
                                                                    4045192
Query
      705
              CACATGGCTGACTACCCCGACTACAAGTACCGGCC
                                              739
             Sbjct
      4045193
>ref|NT_005612.15|Hs3_5769 W Homo sapiens chromosome 3 genomic contig, reference assembly
Length=100530253
                                                  Sort alignments for this subject seq
                                                   E value Score Percent identity
                                                   Query start position Subject star
Features in this part of subject sequence:
  SRY-box 14
Score = 104 bits (114), Expect = 8e-19 Identities = 161/224 (71%), Gaps = 12/224 (5%)
Strand=Plus/Plus
Query
      522
              CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
                                                                     581
              Sbjct
      43978791
                                                                     43978850
      582
              \tt ATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG---CAAACGC
Query
                                                                     638
                         GCCCAGGAAAACCCCAAGATGCACAACTCGGAGATCAGCAAACGCCTAGGTGCCGAA-
      43978851
                                                                     43978907
Sbjct
Query
              TGGAAGCTGC--TCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTG
                                                                     695
                                         Sbjct
      43978908
              TĠĠĂĠĊŤŦĊŦĠŤĊCĠĂĠĠĊĂ--ĠĀĠĂĀĠĊĠĠĊĊĀŤĀĊĀ-ŤĊĠĀŤĠĀĀĠĊCĀĀĠĊĠĠĊŤĀ
                                                                     43978964
Query
      696
              CGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
                                                       739
                  11
                                 CGCGCCCAGCACATGAAGGAGCACCCTGACTACAAGTACCGACC
      43978965
                                                       43979008
Sbjct
Features in this part of subject sequence:
  sex-determining region Y-box 2
Score = 91.5 bits (100), Expect = 5e-15 Identities = 153/219 (69%), Gaps = 2/219 (0%)
Strand=Plus/Plus
              TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG
Query 526
```

```
87925420
                  TCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCC
                                                                                         87925479
Sbjct
                   Query
       586
       87925480
                                                                                         87925539
Sbjct
       646
                   TGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAAG
                                                                                          704
Query
                            Sbjct 87925540
                   ŤŦŦŤĠŦĊĠĠŔĠŔĊĠĠŔĠŔŔĠĊĠĠĊĠŤŤĊŔ~ŤĊĠŔĊĠŔĠĊŦĸŔĠĊĠĠĊŤĠĊĠŔĠĠĊŦĠ
                                                                                         87925598
Query
       705
                   CACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG
                  Sbjct
       87925599
                                                                87925637
Features flanking this part of subject sequence: 1479986 bp at 5' side: similar to PRO0419 371407 bp at 3' side: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 isofor...
Score = 46.4 bits (50), Expect = 0.18 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Minus
Query 2228
                   CATCACCACCTTGGTTTTGTTTTATTTTGCTTCTT 2262
Sbjct 51912243 CATCATCACTTTGGTTATGTTTTGTTTCTT 51912209
Features flanking this part of subject sequence: 680379 bp at 5' side: butyrylcholinesterase precursor 554392 bp at 3' side: hypothetical protein
Score = 42.8 bits (46), Expect = 2.2 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Minus
                   ATTGTTGTTATTGATGTTGTTGATG 2082
Query 2055
                   Sbjct 72724377 ATTGTTGTTGTTGTTGTTGTTGATG 72724350
Features flanking this part of subject sequence:
   51277 bp at 5' side: nuclear factor of kappa light polypeptide gene enhancer i... 83898 bp at 3' side: hypothetical protein
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG 2082
                  Sbjct 8124638 TTGTTGTTTTTTGTTGTTGTTGATG 8124664
Features in this part of subject sequence:
   hypothetical protein
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATG
                                                   2082
                   Sbjct 20900949 TTGTTGTTATTGCTGTTGTTGTTGTTG
Features flanking this part of subject sequence: 1323998 bp at 5' side: hypothetical protein LOC131149 371774 bp at 3' side: similar to hCG2021878
 Score = 41.0 bits (44), Expect = 7.5 Identities = 33/40 (82%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
                   TTCTCTCTTTACCCACCTCCGCCCCTGCGAGGAGTTGAGG
Query 180
                                                                   219
Sbjct 69040917 TTCTCTCTTTACACCACTCAGCCGCTGCCAGGGGTTGAGG
```

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Features flanking this part of subject sequence:
40760 bp at 5' side: leucine rich repeat containing 31
8896 bp at 3' side: sterile alpha motif domain containing 7
Score = 41.0 bits (44), Expect = 7.5 Identities = 31/37 (83\%), Gaps = 0/37 (0\%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTGATGTTGTTGATGGCAAAAAAA
                 TTGTTGTTGTTGTTGTTGTTCTGAAAATAA
Sbjct
       76123541
                                                          76123505
>ref|NW_001842405.1|HsX_WGA1366_36 W Homo sapiens chromosome X genomic contig, alternate ass
(based on HuRef SCAF_1103279188404)
Length=3857110
                                                          Sort alignments for this subject seq E value Score Percent identity
                                                             Query start position Subject star
 Features in this part of subject sequence:
   SRY (sex determining region Y)-box 3
 Score = 100 bits (110), Expect = 9e-18 Identities = 154/216 (71%), Gaps = 8/216 (3%)
 Strand=Plus/Minus
       528
                AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT---CATG
Query
                AAACGCCCATGAACGCCTTCATGGTATGGTCCCGCGGGCAGCGCGCAAAATGGCCCTG
                                                                                3649251
Sbjct
       3649310
       585
                GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAG
Query
                         1111
                GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCGCCGACTGGAAA
Sbjct
       3649250
                                                                                3649194
       645
                CTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAA
                                                                                703
Query
                ĊŢĠĊŢĠĂĊĠĂĊĠĊĠĂĠĂĠĠĊĠĀĊĀŤŢĊĂŢ~ĊĠĀĊĠĀĠĠĊĊĀĀĠĊĠĀĊŢŢĊĠĊĠĊĊŢŢ
       3649193
                                                                                3649135
Sbjct
       704
                GCACATGGCTGACTACCCCGACTACAAGTACCGGCC
Query
                        GCACATGAAGGAGTATCCGGACTACAAGTACCGACC
       3649134
                                                       3649099
Sbjct
 Features flanking this part of subject sequence:
   166860 bp at 5' side: zinc finger protein of the cerebellum 3 893562 bp at 3' side: fibroblast growth factor 13 isoform 1A
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
Query
       2048
               ACCTGTGATTGTTGTTGTTGTTGTTG
                                                  2079
               ACCTGTGATAGTTTTTGTTGTTGTTGTTG
       882950
                                                  882981
Sbjct
>ref|NT_011786.15|HsX_11943 🎆 Homo sapiens chromosome X genomic contig, reference assembly
Length=27718692
                                                           Sort alignments for this subject seq
                                                             E value Score Percent identity
                                                             Query start position Subject star
 Features in this part of subject sequence:
   SRY (sex determining region Y)-box 3
 Score = 100 bits (110), Expect = 9e-18 Identities = 154/216 (71%), Gaps = 8/216 (3%)
 Strand=Plus/Minus
Query
                 AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT---CATG
       528
                 AAACGGCCCATGAACGCCTTCATGGTATGGTCCCGCGGGCAGCGCGCAAAATGGCCCTG
Sbjct
       23798156
                                                                                 23798097
                 GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAG
Query
       585
                                                                                 644
```

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GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCGCCGACTGGAAA
      23798096
                                                                             23798040
Sbjct
                CTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAA
                                                                             703
Query
      645
                             ĊŢĠĊŢĠĂĊĠĂĊĠĊĠĂĠĂĠĠĠŖĊĊĸŢŢĊŔŢĿĠĠĸĠĠĠĠĊĸĸĠĊĠĸĊŢŢĊĠĊĠĊĊŢ
                                                                             23797981
Sbjct
      23798039
      704
                GCACATGGCTGACTACCCCGACTACAAGTACCGGCC
                                                     739
Query
                23797980
                                                     23797945
Sbjct
Features in this part of subject sequence:
  dedicator of cytokinesis 11
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Minus
               GCCTCGGCCTCCGCCAGCC
Query 1149
               1898025
                                           1897999
Sbjct
Features flanking this part of subject sequence:
1062887 bp at 5' side: glutamate dehydrogenase 2
1072247 bp at 3' side: glutamate receptor 3 isoform flop precursor
Score = 41.0 bits (44), Expect = 7.5 Identities = 33/40 (82%), Gaps = 0/40 (0%)
Strand=Plus/Minus
Query 2056
               TTGTTGTTATTGATGTTGTTGATGGCaaaaaaaaaaaaa
               TTGTTGTTGTTGTTGTTGTTTTTCAGAAAACAAA
Sbjct
      5457504
Features flanking this part of subject sequence: 168026 bp at 5' side: zinc finger protein of the cerebellum 3
   894725 bp at 3' side: fibroblast growth factor 13 isoform 1B
Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
                ACCTGTGATTGTTGTTTGTTGTTGTTG
      2048
Query
                21031603
                                                 21031634
Sbjct
>ref|NT_027140.6|Hs13_27300 Memory Homo sapiens chromosome 13 genomic contig, reference assembly
Length=1821999
                                                       Sort alignments for this subject seq E value Score Percent identity
                                                         Query start position Subject star
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 1
Score = 96.9 bits (106), Expect = 1e-16 Identities = 152/215 (70%), Gaps = 2/215 (0%)
Strand=Plus/Plus
Query
      526
              TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG
               TCAAACGGCCATGAACGCCTTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGGCCC
      218130
                                                                           218189
Sbjct
Query
      586
              AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAAGC
                                                                           645
              218190
                                                                           218249
Sbjct
      646
              TGCTCAAAGACAGCGACAAGATCCCTTTCATTCGA-GAGGCGGAGCGGCTGCGCCTCAAG
                                                                           704
Query
                           TCATGTCCGAGGCCGAGAAGCGGCCGTTCA-TCGACGAGGCCAAGCGGCTGCGCGCGCTG
      218250
                                                                           218308
Sbjct
              CACATGGCTGACTACCCCGACTACAAGTACCGGCC
Query
      705
```

```
218309 CACATGAAGGAGCACCCGGATTACAAGTACCGGCC 218343
Features flanking this part of subject sequence: 269051 bp at 5' side: SRY (sex determining region Y)-box 1
   38475 bp at 3' side: hypothetical protein LOC122258
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
               TTGTTGTTATTGATGTTGTTGATG
                                             2082
               488205
               TTGTTGTTGATGTTGTTGTTG
                                             488231
Sbjct
>ref|NW_001838745.1|Hs22_WGA1304_36 Momo sapiens chromosome 22 genomic contig, alternate a
(based on HuRef SCAF_110\overline{3}2791883\overline{7}2)
Length=21026802
                                                           Sort alignments for this subject seq
                                                             E value Score Percent identity
                                                             Query start position Subject star
Features in this part of subject sequence:
   SRY (sex determining region Y)-box 10
 Score = 95.1 bits (104), Expect = 4e-16 Identities = 94/122 (77%), Gaps = 0/122 (0%)
 Strand=Plus/Minus
Query
       521
                 GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT
                 16472614
                 GCACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGGCTCAGGCAGCGCGCAGGAAGCT
                                                                                 16472555
Sbjct
       581
                 CATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG
                                                                                  640
Query
                 16472554
                                                                                 16472495
Sbjct
Query
                 GA
Sbjct
     16472494
                 GΑ
                    16472493
 Features in this part of subject sequence:
   SRY (sex determining region Y)-box 10
 Score = 77.0 bits (84), Expect = 1e-10 Identities = 79/101 (78%), Gaps = 2/101 (1%)
 Strand=Plus/Minus
Query
       644
                 GCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGAG-AGGCGGAGCGGCTGCGCCTCA
                 16467270
                                                                                 16467212
Sbict
       703
                 AGCACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG
Query
                 16467211
Features flanking this part of subject sequence: 22174 bp at 5' side: like-glycosyltransferase 1289151 bp at 3' side: intestine-specific homeobox
 Score = 42.8 bits (46), Expect = 2.2 Identities = 25/26 (96%), Gaps = 0/26 (0%)
 Strand=Plus/Plus
                                              2081
Query 2056
                 TTGTTGTTATTGATGTTGTTGAT
                 Sbjct 12263566
                                              12263591
 Features in this part of subject sequence:
   calcineurin binding protein 1
 Score = 41.0 bits (44), Expect = 7.5
```

```
Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
      2056
               TTGTTGTTATTGATGTTGTTGATGGCAAA
Query
               TTGTTGTTGTTGTTGTTGTTGGTAAA
      2585440
Sbjct
>ref|NT_011520.11|Hs22_11677 Momo sapiens chromosome 22 genomic contig, reference assembly
Length=23276302
                                                      Sort alignments for this subject seq
                                                        E value Score Percent identity
                                                        Query start position Subject star
Features in this part of subject sequence:
   SRY (sex determining region Y)-box 10
Score = 95.1 bits (104), Expect = 4e-16 Identities = 94/122 (77%), Gaps = 0/122 (0%)
 Strand=Plus/Minus
                GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT
Query 521
                                                                            580
                1 111
      17770001
                GCACGTCAAGCGCCCATGAACGCCTTCATGGTGTGGGCTCAGGCAGCGCGCAGGAAGCT
                                                                           17769942
Sbjct
Query
      581
                CATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG
                                                                            640
                                CGCGGACCAGTACCCGCACCTGCACAACGCTGAGCTCAGCAAGACGCTGGGCAAGCTCTG
      17769941
                                                                           17769882
Sbjct
                GΑ
                    642
Query
Sbjct
      17769881
                GΑ
                   17769880
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 10
 Score = 77.0 bits (84),
                       Expect = 1e-10
 Identities = 79/101 (78%), Gaps = 2/101 (1%)
 Strand=Plus/Minus
Query 644
                GCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGAG-AGGCGGAGCGGCTGCGCCTCA
                Sbjct
      17764657
                                                                           17764599
                AGCACATGGCTGACTACCCCGACTACAAGTACCGGCCCAGG
Query
                17764558
Sbjct
      17764598
Features flanking this part of subject sequence: 22175 bp at 5' side: like-glycosyltransferase 1283418 bp at 3' side: intestine-specific homeobox
 Score = 42.8 bits (46), Expect = 2.2
 Identities = 25/26 (96%), Gaps = 0/26 (0%)
 Strand=Plus/Plus
Query
      2056
                TTGTTGTTATTGATGTTGTTGAT
                                           2081
                TTGTTGTTATTGTTGTTGTTGAT
     13570207
                                           13570232
Sbjct
Features in this part of subject sequence:
  calcineurin binding protein 1
Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
      2056
               TTGTTGTTATTGATGTTGTTGATGGCAAA
Query
               3900601
               TTGTTGTTGTTGTTGTTGTTGTTAAA
                                               3900632
```

>ref|NW_001839122.2|Hs8_WGA515_36 Homo sapiens chromosome 8 genomic contig, alternate asse (based on HuRef SCAF 1103279188150)

```
Length=4000776
```

```
Features in this part of subject sequence:
  SRY-box 7
Score = 87.8 bits (96), Expect = 6e-14 Identities = 63/72 (87%), Gaps = 3/72 (4%)
 Strand=Plus/Plus
              GAGGCGGAGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC-
                                                                        739
Query 681
               GAGGCGGAGCGCTGCGCCTGCAGCACATGCAGGACTACCCCAACTACAAGTACCGGCCG
      1473842
Sbjct
      740
               --CAGGAAGAAG
                           749
Query
                CGCAGGAAGAAG
Sbjct
      1473902
                           1473913
Features in this part of subject sequence:
  SRY-box 7
Score = 53.6 bits (58), Expect = 0.001 Identities = 73/102 (71%), Gaps = 0/102 (0%)
 Strand=Plus/Plus
Query 530
              GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCA
              Sbjct
      1470162
      590
Query
              GTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG
                                                       631
                     GAACCCGGACCTGCACAACGCCGAGCTCAGCAAGATGCTGGG
Sbjct
      1470222
>ref|NT_077531.3|Hs8_77580 W Homo sapiens chromosome 8 genomic contig, reference assembly
Length=4537293
                                                     Sort alignments for this subject seq
                                                      E value Score Percent identity
                                                      Query start position Subject star
Features in this part of subject sequence:
  SRY-box 7
Score = 87.8 bits (96), Expect = 6e-14 Identities = 63/72 (87%), Gaps = 3/72 (4%)
 Strand=Plus/Minus
      681
               GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC-
                                                                        739
Query
               GÁGGCGGÁGCGCTGCGCCTGCÁGCÁCÁTGCAGGÁCTÁCCCAÁCTÁCÁÁGTÁCCGGCCG
Sbjct
      3059477
                                                                        3059418
      740
               --CAGGAAGAAG
Query
                           749
                3059417
              CGCAGGAAGAAG
                           3059406
Sbjct
Features in this part of subject sequence:
  SRY-box 7
Score = 53.6 bits (58), Expect = 0.001 Identities = 73/102 (71%), Gaps = 0/102 (0%)
Strand=Plus/Minus
Query 530
              GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGCGCAAGATCATGGAGCA
                                                                        589
              3063157
Sbjct
      590
              GTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGG
Query
                                                       631
                     GAACCCGGACCTGCACAACGCCGAGCTCAGCAAGATGCTGGG
Sbjct
```

>ref|NW_001838339.2|Hs16_WGA937_36 Momo sapiens chromosome 16 genomic contig, alternate as

```
(based on HuRef SCAF 1103279188181)
Length=2624016
```

```
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 8
Score = 86.0 bits (94), Expect = 2e-13 Identities = 83/107 (77%), Gaps = 0/107 (0%)
Strand=Plus/Minus
              AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAG
      528
Query
              ÁÁĞĊĠĠĊĊĊĂŢĠĂĂĊĠĊĂŢŢĊĂŢĠĠŢĠŢĠĠĠĊĠĊĠĠĠĠĠĊĠĊĠĊĀĀĠĊŢĠĠĊĠĂĊ
      1665887
                                                                       1665828
Sbjct
Query
      588
              CAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAA 634
              CAGTACCCGCACCTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAA
Sbjct
      1665827
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 8
Score = 53.6 bits (58), Expect = 0.001 Identities = 71/99 (71%), Gaps = 6/99 (6%)
 Strand=Plus/Minus
              GAGGCGGAGCGGCTCCAAGCACATGGCTGACTACCCCGACTACAAGTAC-----
Query
     681
              1664351
              ĠĂĠĠĊĀĠĀĠĊĠĊĊŤŦĊĠĊĠŦĠĊĀĠĊĀĊĀĀĠĀĀĠĠĀĊĊĀĊĊĊĠĀĊŦĀĊĀĀĠŦĀĊĊĀĠĊĊĀ
                                                                       1664292
Sbjct
Query
      735
              CGGCCCAGGAAGAGGTGAAGTCCGGCAACGCCAACTCC
                                                    773
              Sbjct 1664291
              CGGCGCAGGAAGAGCGCCAAAGCCGGCCACAGCGACTCC
                                                    1664253
>ref|NT_037887.4|Hs16_37891 > Homo sapiens chromosome 16 genomic contig, reference assembly
Length=8576922
                                                    Sort alignments for this subject seq
                                                      E value Score Percent identity
                                                      Query start position Subject star
 Features in this part of subject sequence:
  SRY (sex determining region Y)-box 8
Score = 86.0 bits (94), Expect = 2e-13 Identities = 83/107 (77%), Gaps = 0/107 (0%)
 Strand=Plus/Plus
Query 528
             AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAG
             ÄÄĞÇĞĞÇÇÇÄTĞÄÄÇĞÇATTÇATĞĞTĞTĞĞĞÇĞÇĞÇĞÇĞÇĞÇĞÇĞÇÂÄĞÇTĞGCÇĞÂÇ
      972230
Query
      588
             CAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAA
             Sbjct 972290
Features in this part of subject sequence:
  SRY (sex determining region Y)-box 8
Score = 53.6 bits (58), Expect = 0.001 Identities = 71/99 (71%), Gaps = 6/99 (6%)
Strand=Plus/Plus
             GAGGCGGAGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTAC-----
      681
Query
             973766
Sbjct
Query
      735
             CGGCCCAGGAAGAGGTGAAGTCCGGCAACGCCAACTCC
             CGGCGCAGGAAGAGCGCCAAAGCCGGCCACAGCGACTCC
      973826
                                                   973864
```

Sbjct

```
(based on HuRef SCAF_1103279188157)
Length=37103761
                                                             Sort alignments for this subject seq
                                                               E value Score Percent identity
                                                               Query start position Subject star
 Features in this part of subject sequence:
   SRY-box 13
 Score = 77.0 bits (84), Expect = 1e-10 Identities = 73/91 (80%), Gaps = 2/91 (2%)
                          Expect = 1e-10
 Strand=Plus/Minus
Query 522
                 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGCGCAAGATC
                1847108
Sbjct
       582
                ATGGA-GCAGTCGCCCGACATGCACAACGCC
Query
                                                    611
                           CTGCAAGCCTTC-CCAGACATGCACAACTCC
Sbjct 1847048
Features in this part of subject sequence:
   protein phosphatase 1, regulatory (inhibitor) subunit 12B... protein phosphatase 1, regulatory (inhibitor) subunit 12B...
 Score = 46.4 bits (50), Expect = 0.18
 Identities = 34/40 (85%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTGTTGTTGTTGTTTAAAAAAAAAAAAAAA
Sbjct 3618816
                                                              3618777
 Features in this part of subject sequence:
   protein phosphatase 1, regulatory (inhibitor) subunit 12B... protein phosphatase 1, regulatory (inhibitor) subunit 12B...
 Score = 46.4 bits (50), Expect = 0.18
 Identities = 34/40 (85%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATGGCaaaaaaaaaaaaa
                                                              2095
                 TTGTTGTTGTTGTTGTTGTTGTTTAAAAAAAAA
Sbjct 3618819
                                                             3618780
 Features flanking this part of subject sequence:
   76699 bp at 5' side: chromosome 1 open reading frame 21 327829 bp at 3' side: hypothetical protein LOC116461
 Score = 42.8 bits (46), Expect = 2.2
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATGG
                                                  2083
                  Sbjct 21499677 TTGTTGTTGTTGTTGTTGTTGATGG
                                                 21499650
Features flanking this part of subject sequence: 1296333 bp at 5' side: regulator of G-protein signalling 18 409014 bp at 3' side: family with sequence similarity 5, member C
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
                  TTGTTGTTATTGATGTTGTTGATG
Query 2056
                                                 2082
                   TTGTTGTTATTGTTGTTGTTGTTG
                                                15037598
Sbjct 15037624
Features in this part of subject sequence:
```

>ref|NW_001838533.2|Hs1_WGA129_36 💹 Homo sapiens chromosome 1 genomic contig, alternate asse

```
hypothetical protein
```

```
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2423
                 CCttttttCCTCCCTCTTTTCCCCTT
                                              2449
                 CCATTTTTCCTGCCTCTTTTCCCCTT
Sbjct 28353580
                                              28353606
 Features in this part of subject sequence:
   astrotactin isoform 1
 Score = 41.0 bits (44),
                         Expect = 7.5
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus
Query 2290
                 GCACCCTedecedetttttt
                 28766569
                 GCACCCTCCCCCCTTTTTTT
                                         28766590
Sbjct
>ref|NW_001838085.1|Hs13_WGA794_36 Momo sapiens chromosome 13 genomic contig, alternate as
(based on HuRef SCAF_1103279188104)
Length=1807819
                                                         Sort alignments for this subject seq E value Score Percent identity
                                                           Query start position Subject star
Features flanking this part of subject sequence: 287495 bp at 3' side: hypothetical protein LOC122258
 Score = 77.0 bits (84), Expect = 1e-10 Identities = 80/105 (76%), Gaps = 0/105 (0%)
 Strand=Plus/Plus
               TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG
Query
       526
               TCAAACGGCCCATGAACGCCTTCATGGTGTGCCCGCGGGCAGCGCGCAAGATGGCCC
Sbjct
       226768
                                                                              226827
               AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGG
Query
       586
                                                              630
                       AGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGG
Sbjct
       226828
                                                               226872
 Features flanking this part of subject sequence:
   39257 bp at 3'side: hypothetical protein LOC122258
 Score = 41.0 bits (44),
                        Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
               TTGTTGTTATTGATGTTGTTGATG
               475084
Sbjct
>ref|NT 004487.18|Hs1 4644 💹 Homo sapiens chromosome 1 genomic contig, reference assembly
Length=56413061
                                                         Sort alignments for this subject seq
                                                           E value Score Percent identity
                                                           Query start position Subject star
Features in this part of subject sequence:
   SRY-box 13
 Score = 77.0 bits (84), Expect = 1e-10 Identities = 73/91 (80%), Gaps = 2/91 (2%)
 Strand=Plus/Plus
Query 522
                 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
                                                                                581
                 Sbjet 54583178 CÁCATCAAGAGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGATC
                                                                                54583237
```

```
Query 582
                   ATG-GAGCAGTCGCCCGACATGCACAACGCC
Sbjct 54583238 CTGCAAGCCTTC-CCAGACATGCACAACTCC
 Features in this part of subject sequence:
   protein phosphatase 1, regulatory (inhibitor) subunit 12B... protein phosphatase 1, regulatory (inhibitor) subunit 12B...
 Score = 46.4 bits (50), Expect = 0.18 Identities = 34/40 (85%), Gaps = 0/40 (0%)
 Strand=Plus/Plus
Query 2056
                   Sbjct 52810695
                                                                    52810734
 Features in this part of subject sequence:
   protein phosphatase 1, regulatory (inhibitor) subunit 12B... protein phosphatase 1, regulatory (inhibitor) subunit 12B...
 Score = 46.4 bits (50), Expect = 0.18 Identities = 34/40 (85%), Gaps = 0/40 (0%)
 Strand=Plus/Plus
                   Query 2056
                                                                    2095
                    Features flanking this part of subject sequence: 327837 bp at 5' side: hypothetical protein LOC116461
   76799 bp at 3' side: chromosome 1 open reading frame 21
 Score = 42.8 bits (46), Expect = 2.2 Identities = 26/28 (92\%), Gaps = 0/28 (0\%)
 Strand=Plus/Plus
                   TTGTTGTTATTGATGTTGTTGATGG
Query 2056
                    Sbjct 34860172 TTGTTGTTGTTGTTGTTGTTGATGG
                                                      34860199
 Features in this part of subject sequence:
   astrotactin isoform 1
   astrotactin isoform 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Minus
Query 2290
                   GCACCCTocccccctttttt
                                               2311
Sbjct 27602408 GCACCCTCCCCCCTTTTTT
                                               27602387
 Features in this part of subject sequence:
   hypothetical protein
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
                   CCttttttCCCTCTTTTCCCCTT
Query 2423
Sbjct 28014783
                   CCATTTTTCCTGCCTCTTTTCCCCTT
Features flanking this part of subject sequence:
409150 bp at 5' side: family with sequence similarity 5, member C
1294572 bp at 3' side: regulator of G-protein signalling 18
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
```

```
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG
                                              2082
                 Sbjct 41323524
                                              41323550
Features flanking this part of subject sequence:
409171 bp at 5' side: family with sequence similarity 5, member C
1294551 bp at 3' side: regulator of G-protein signalling 18
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Plus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG
                                              2082
                 Sbjct 41323545
                                              41323571
>ref|NW_001839132.1|Hs8_WGA525_36 Nome aspiens chromosome 8 genomic contig, alternate asse
(based on HuRef SCAF_1103279188282)
Length=30141836
                                                          Sort alignments for this subject seq
                                                           E value Score Percent identity
                                                           Query start position Subject star
 Features in this part of subject sequence:
   SRY-box 17
 Score = 66.2 bits (72), Expect = 2e-07 Identities = 50/59 (84%), Gaps = 0/59 (0%)
 Strand=Plus/Plus
Query 681
                GAGGCGGAGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
                                                                              739
                7238558 GAGGCAGAGCGGCTGCGCGTGCAGCACATGCAGGACCACCCCAACTACAAGTACCGGCC
                                                                              7238616
Sbict
 Features in this part of subject sequence:
   SRY-box 17
 Score = 55.4 bits (60), Expect = 3e-04 Identities = 76/105 (72%), Gaps = 6/105 (5%)
 Strand=Plus/Plus
       530
                GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG---A
Query
                7237795
                                                                               7237851
Sbjct
       587
                GCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG
Query
                       | \cdot | \cdot |
                                                        +++++
                GCAGAATCCAGACCTGCACAACGCCGAGTTGAGCAAGATGCTGGG
Sbjct
       7237852
                                                                7237896
 Features in this part of subject sequence:
   hypothetical protein LOC23514
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
               TTGTTGTTATTGATGTTGTTGATG
                                            2082
              Sbjct 497262
                                            497288
 Features in this part of subject sequence:
   hypothetical protein LOC23514
 Score = 41.0 bits (44),
                        Expect = 7.5
 Identities = 30/35 (85%), Gaps = 0/35 (0%)
 Strand=Plus/Plus
Query 2051
               TGTGATTGTTATTGATGTTGTTGATGGCA
               497266
               TGTTATTGTTGTTGTTGTTGTTGTTGTTGACA
                                                    497300
Sbjct
```

```
Features flanking this part of subject sequence: 63747 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ... 181279 bp at 3' side: similar to hCG1799828
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATG
                   Sbjct 27230124 TTGTTGTTATTGTTGTTGTTGTTGTTG
                                                   27230098
Features flanking this part of subject sequence: 473228 bp at 5' side: cysteine-rich secretory protein LCCL domain containing 1 33133 bp at 3' side: hepatocyte nuclear factor 4, gamma
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATG 2082
                   Sbjct 28305493 TTGTTGTTGTTGTTGTTGTTGATG
                                                   28305467
>ref|NT_008183.18|Hs8_8340 Memo sapiens chromosome 8 genomic contig, reference assembly
Length=38454502
                                                                Sort alignments for this subject seq
                                                                   E value Score Percent identity
                                                                   Query start position Subject star
 Features in this part of subject sequence:
   SRY-box 17
 Score = 66.2 bits (72), Expect = 2e-07 Identities = 50/59 (84%), Gaps = 0/59 (0%)
 Strand=Plus/Plus
Query 681
                  GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
                  Sbjet 7225020 GAGGCAGAGCGGCTGCGCGTGCAGCATGCAGGACCACCCCAACTACAAGTACCGGCC
                                                                                       7225078
Features in this part of subject sequence:
   SRY-box 17
 Score = 55.4 bits (60), Expect = 3e-04 Identities = 76/105 (72%), Gaps = 6/105 (5%)
 Strand=Plus/Plus
Query
       530
                  GCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG---A
                  ĠĊĠĠĊĊĠĂŢĠĂĀĊĠĊŢŢŢĊĂŢĠĠŢĠŢĠĠĠĊŢĀĀĠĠĀĊĠĂ——ĠĊĠĊĀĀĠĊĠĠĊŢĠĠĊĠĊĀ
       7224257
                                                                                        7224313
Sbjct
       587
                  GCAGTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGG
Query
                          7224314 GCAGAATCCAGACCTGCACAACGCCGAGTTGAGCAAGATGCTGGG
Features flanking this part of subject sequence: 63856 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ... 184610 bp at 3' side: similar to hCG1799828 isoform 1
 Score = 42.8 bits (46), Expect = 2.2 Identities = 31/36 (86%), Gaps = 0/36 (0%)
 Strand=Plus/Minus
Query 2051
                   TGTGATTGTTATTGATGTTGTTGTTGATGGCAA 2086
                   Sbjct 27193847 TGTTATTGTTGTTGTTGTTGTTGTTGTTAGCAA 27193812
 Features in this part of subject sequence:
```

hypothetical protein LOC23514

```
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Plus
Query 2056
               TTGTTGTTATTGATGTTGTTGATG
                                             2082
               TTGTTGTTATTGTTGTTGTTGTTG
       488931
Sbjct
 Features in this part of subject sequence:
   hypothetical protein LOC23514
 Score = 41.0 bits (44), Expect = 7.5 Identities = 30/35 (85%), Gaps = 0/35 (0%)
 Strand=Plus/Plus
Query 2051
               TGTGATTGTTGTTGATGTTGTTGATGGCA
               Sbict
       488935
               TGTTATTGTTGTTGTTGTTGTTGTTGACA
                                                     488969
 Features flanking this part of subject sequence:
   63869 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ... 184606 bp at 3' side: similar to hCG1799828 isoform 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG
                                               2082
                 Sbjct 27193851
                 TTGTTGTTATTGTTGTTGTTGTTG
                                               27193825
Features flanking this part of subject sequence:
   474603 bp at 5' side: cysteine-rich secretory protein LCCL domain containing 1 33122 bp at 3' side: hepatocyte nuclear factor 4, gamma
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG
                                               2082
                 28272460
                 TTGTTGTTGTTGTTGTTGATG
Sbjct
>ref|NW_001842422.1|HsY_WGA1383_36 Momo sapiens chromosome Y genomic contig, alternate ass
(based on HuRef SCAF_1103279188414)
Length=3942718
                                                           Sort alignments for this subject seq E value Score Percent identity
                                                             Query start position Subject star
 Features in this part of subject sequence:
   sex determining region Y
 Score = 64.4 bits (70), Expect = 7e-07
 Identities = 94/126 (74%), Gaps = 8/126 (6%)
 Strand=Plus/Minus
Query
       528
             AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCGCAAGAT---CAT
             AAGCGACCATGAACGCATTCATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT
       8468
                                                                              8410
Sbjct
Query
       584
             GGAGCAGTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA
                                                                             643
             8409
Sbjct
             GCTGCT
       644
                     649
Query
             AATGCT
Sbjct
       8352
                     8347
```

Features flanking this part of subject sequence:

```
770513 bp at 5' side: TGFB-induced factor homeobox 2-like, Y-linked 776921 bp at 3' side: hypothetical protein
 Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus
Query 1149
                GCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGCA
                Sbjct 1579134
               GCCTCGGCCTCTGCCTCCACCTCAGCCTCTGCCTCCACA
>ref|NT_011896.9|HsY_12053 MM Homo sapiens chromosome Y genomic contig, reference assembly
Length=6265435
                                                         Sort alignments for this subject seq
                                                           E value Score Percent identity
                                                           Query start position Subject star
 Features in this part of subject sequence:
   sex determining region Y
 Score = 64.4 bits (70), Expect = 7e-07
 Identities = 94/126 (74%), Gaps = 8/126 (6%)
 Strand=Plus/Minus
                                                                           583
Query 528
            AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCGCAAGAT---CAT
             AAGCGACCCATGAACGCATTCATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT
       5944
                                                                           5886
Sbjct
       584
             GGAGCAGTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA
Query
                                                                           643
                         AĞAĞ-AATC-CCAĞA-ATĞCGAAACTCAĞAĞATCAĞCAAĞCAĞCTĞĞĞATACCAĞTĞĞAA
       5885
Sbjct
      644
             GCTGCT
Query
               1111
Sbjct
       5828
            AATGCT
                    5823
Features flanking this part of subject sequence: 675817 bp at 5' side: TGFB-induced factor homeobox 2-like, Y-linked 777040 bp at 3' side: protocadherin 11 Y-linked isoform a
                        Expect = 0.62
 Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus
                GCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGCA
Query 1149
                                                        1187
                GCCTCGGCCTCTGCCTCCACCTCAGCCTCTGCCTCCACA
Sbjct 1474178
                                                        1474140
 Features in this part of subject sequence:
   transducin beta-like 1Y
   transducin beta-like 1Y
 Score = 42.8 \text{ bits } (46),
                        Expect = 2.2
 Identities = 31/36 (86%), Gaps = 0/36 (0%)
 Strand=Plus/Plus
Query 2047
                GACCTGTGATTGTTGTTGTTGATGTTGTTGATG
                                                      2082
                        GAACTGTTTTTGTTGTTATTGTTGTTGTTGTTG
Sbjct 4284860
                                                      4284895
Features in this part of subject sequence:
   transducin beta-like 1Y
   transducin beta-like 1Y
 Score = 41.0 bits (44),
                        Expect = 7.5
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
Query 2051
                TGTGATTGTTGTTGATGTTGTTGATG
                4284873
                TGTTATTGTTGTTGTTGTTGTTGTTG
                                                  4284904
Sbjct
```

```
>ref|NT_011333.5|Hs20_11490 *** Homo sapiens chromosome 20 genomic contig, reference assembly
Length=1702150
                                                       Sort alignments for this subject seq
                                                         E value Score Percent identity
                                                         Query start position Subject star
Features in this part of subject sequence:
  hypothetical protein
  SŘÝ-box 18
Score = 62.6 bits (68), Expect = 2e-06 Identities = 83/114 (72%), Gaps = 6/114 (5%)
Strand=Plus/Minus
Query
      521
               GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGCGCAAGAT
               GCGCATCCGGCGGCCCATGAACGCCTTCATGGTGTGGGCAAAGGACGA-
Sbjct
      581
               CATGG---AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG
Query
               Sbjct
      1417194
Features in this part of subject sequence:
  hypothetical protein
   SRY-box 18
Score = 53.6 bits (58), Expect = 0.001 Identities = 47/59 (79%), Gaps = 0/59 (0%)
 Strand=Plus/Minus
Query 681
               GAGGCGGAGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
                                               GAAGCCGAACGGCTGCGCGTGCAGCACTTGCGCGACCACCCCAACTACAAGTACCGGCC
Sbjct
     1416895
                                                                          1416837
>ref|NW_001838052.1|Hs12_WGA761_36 Memo sapiens chromosome 12 genomic contig, alternate as
(based on HuRef SCAF_1103279188408)
Length=21675488
                                                       Sort alignments for this subject seq
                                                         E value Score Percent identity
                                                         Query start position Subject star
Features in this part of subject sequence:
   SRY (sex determining region Y)-box 5 isoform c
   SRY (sex determining region Y)-box 5 isoform b
Score = 57.2 bits (62), Expect = 1e-04 Identities = 76/103 (73%), Gaps = 2/103 (1%)
 Strand=Plus/Minus
Query 522
                CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT
                                                                            580
                CACÁTAAAGCGTCCAATGAATGCCTTCATGGTGTGGGCTAAAGAT-GAACGGAGAAAGAT
      14103106
                                                                            14103048
Sbjct
                CATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAG
      581
Query
                         CCTTCAAGCCTTTCCTGACATGCACAACTCCAACATCAGCAAG
Sbjct
     14103047
                                                            14103005
Features flanking this part of subject sequence:
   15642 bp at 5' side: hypothetical protein LOC440087 585 bp at 3' side: hypothetical protein LOC144608
Score = 42.8 bits (46), Expect = 2.2 Identities = 29/33 (87\%), Gaps = 0/33 (0\%)
 Strand=Plus/Minus
      2050
               CTGTGATTGTTGTTGATGTTGTTGATG
Query
               5384229
               CTGTGTTGTTGTTGTTGTTGTTGTTG
                                                 5384197
Sbjct
Features flanking this part of subject sequence:
   70138 bp at 5' side: pleckstrin homology domain containing, family A member 5
```

```
463 bp at 3' side: AE binding protein 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query 1144
                  CCAGCGCCTCGGCCTCCTC
                  Sbjct 10001352
                                                10001328
>ref|NT_009714.16|Hs12_9871 X Homo sapiens chromosome 12 genomic contig, reference assembly
Length=27615668
                                                               Sort alignments for this subject seq
                                                                 E value Score Percent identity
                                                                 Query start position Subject star
 Features in this part of subject sequence:
   SRY (sex determining region Y)-box 5 isoform a
   SRY (sex determining region Y)-box 5 isoform b
Score = 57.2 bits (62), Expect = 1e-04 Identities = 76/103 (73%), Gaps = 2/103 (1%)
 Strand=Plus/Minus
                                                                                       580
Query 522
                  CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT
                  16455227
                                                                                       16455169
Sbict
                  {\tt CATGGAGCAGTCGCCGACATGCACAACGCCGAGATCTCCAAG}
Query
       581
                                                                   623
                                    CCTTCAAGCCTTTCCTGACATGCACAACTCCAACATCAGCAAG
Sbjct 16455168
Features flanking this part of subject sequence: 15639 bp at 5' side: hypothetical protein LOC440087 585 bp at 3' side: hypothetical protein LOC144608
 Score = 42.8 bits (46), Expect = 2.2 Identities = 29/33 (87\%), Gaps = 0/33 (0\%)
 Strand=Plus/Minus
Query 2050
                 CTGTGATTGTTGTTGATGTTGTTGATG
                 Sbjct 7734259 CTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
                                                        7734227
Features in this part of subject sequence:
   pregnancy-zone protein
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Plus
                 TTGTTGTTATTGATGTTGTTGATG
Query 2056
                                                 2082
                 TTGTTGTTATTGTTGTTGTTGTTG
Sbjct 2067054
                                                 2067080
Features flanking this part of subject sequence: 70051 bp at 5' side: pleckstrin homology domain containing, family A member 5 462 bp at 3' side: AE binding protein 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query 1144
                  CCAGCGCCTCGGCCTCCTC
                 12351770
                                                12351746
>ref|NW_001838671.1|Hs20_WGA1230_36 🎆 Homo sapiens chromosome 20 genomic contig, alternate a
(based on HuRef SCAF_1103279188118)
Length=1477768
```

```
Features in this part of subject sequence:
   SRY-box 18
 Score = 53.6 bits (58), Expect = 0.001 Identities = 47/59 (79%), Gaps = 0/59 (0%)
 Strand=Plus/Minus
                 GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC
Query 681
                                                    GÁAGCCGÁACGGCTGCGCGTGCÁGCÁCTTGCGCGÁCCÁCCCAÁCTÁCAÁGTÁCCGGCC
Sbjct 1435018
>ref|NW 001838954.2|Hs5 WGA347 36 💹 Homo sapiens chromosome 5 genomic contig, alternate asse
(based on HuRef SCAF_1103279188298)
Length=20179980
                                                            Sort alignments for this subject seq
                                                              E value Score Percent identity
                                                              Query start position Subject star
 Features flanking this part of subject sequence:
   78951 bp at 5' side: stanniocalcin 2 precursor
3698 bp at 3' side: NK2 transcription factor related, locus 5
 Score = 51.8 bits (56), Expect = 0.004 Identities = 42/50 (84%), Gaps = 2/50 (4%)
 Strand=Plus/Minus
                 \tt CGGACTCCCAGCGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
Query 1137
                                                                       1186
                 Sbjet 2701243 ČĠĠÁĊŤĊĆĠĠĊ--ĊŤĊĠĠĊĊŤĊĊĠĊĊŤĊĊĠĊĊŤĊĊĠĊĊŤĊĊĠĊ
                                                                        2701196
Features in this part of subject sequence:
   slit homolog 3
 Score = 44.6 bits (48), Expect = 0.62 Identities = 32/36 (88%), Gaps = 1/36 (2%)
                         Expect = 0.62
 Strand=Plus/Plus
                 CCtttttttCCTCCCTCTTTTCC-CCTTGCCCCCTC
Query 2423
                                                         2457
                 7061862
                CCTTTTTTCCTCCCTCTTATCCTCCCTTCCCCCTC
                                                         7061897
Sbjct
 Features flanking this part of subject sequence:
   555459 bp at 5' side: msh homeobox 2 60915 bp at 3' side: HMP19 protein
 Score = 42.8 bits (46), Expect = 2.2 Identities = 32/38 (84%), Gaps = 0/38 (0%)
 Strand=Plus/Minus
Query 1999
                 CTCTGCCCAGCCGGAGGACGCGGAGGAGGAAGAGGGT
                                                           2036
                 Sbjct 1770755
                CTCTGCACAGCCGGACAGGTGAGGAGGAGGAGAGAGGGT
                                                           1770718
 Features in this part of subject sequence:
   SRY (sex determining region Y)-box 30 isoform a SRY (sex determining region Y)-box 30 isoform b
 Score = 41.0 bits (44), Expect = 7.5 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Plus
Query 528
                 AAGCGACCCATGAACGCCTTCATGGTGTGG
                                                   557
                  Sbjct 18297850
                 AAGCGACCCATGAACGCATTTATGGTTTGG
                                                   18297879
>ref|NT_011295.10|Hs19_11452 WHomo sapiens chromosome 19 genomic contig, reference assembly
Length=15825424
```

```
Features flanking this part of subject sequence: 1925 bp at 5' side: TRM1 tRNA methyltransferase 1 16847 bp at 3' side: transcriptional repressor NAC1
 Score = 51.8 bits (56), Expect = 0.004 Identities = 34/38 (89%), Gaps = 0/38 (0%)
 Strand=Plus/Minus
Query 1149
                  GCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC
                  Sbjct
        4491977
                                                                 4491940
 Features in this part of subject sequence: calcium channel, alpha 1A subunit isoform 2
   calcium channel, alpha 1A subunit isoform 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGA 2080
                   TTGTTGTTGATGTTGTTGA 4698316
Sbjct
      4698340
>ref|NT_023133.12|Hs5_23289 We Homo sapiens chromosome 5 genomic contig, reference assembly
Length=25714846
                                                                  Sort alignments for this subject seq
                                                                     E value Score Percent identity
                                                                     Query start position Subject star
 Features flanking this part of subject sequence: 3698 bp at 5' side: NK2 transcription factor related, locus 5 79019 bp at 3' side: stanniocalcin 2 precursor
 Score = 51.8 bits (56), Expect = 0.004 Identities = 42/50 (84%), Gaps = 2/50 (4%)
 Strand=Plus/Plus
                   CGGACTCCCAGCGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
Query 1137
                   Sbjct 17475370
                                                                                17475417
 Features in this part of subject sequence:
   slit homolog 3
 Score = 44.6 bits (48),
                            Expect = 0.62
 Identities = 32/36 (88%), Gaps = 1/36 (2%)
 Strand=Plus/Minus
Query 2423
                   CCttttttCCTCCCTCTTTTCC-CCTTGCCCCCTC
Sbjet 13112345 CCTTTTTTCCTCCCTCTTATCCTCCCTTCCCCCTC
                                                               13112310
 Features flanking this part of subject sequence: 60329 bp at 5' side: HMP19 protein 556789 bp at 3' side: msh homeobox 2
 Score = 42.8 bits (46), Expect = 2.2 Identities = 32/38 (84%), Gaps = 0/38 (0%)
 Strand=Plus/Plus
Query 1999
                   CTCTGCCCAGCCGGAGGACGCGGAGGAGGAGGGT
                                                                  2036
Features in this part of subject sequence:
   SRY (sex determining region Y)-box 30 isoform a
   SRY (sex determining region Y)-box 30 isoform b
```

```
Score = 41.0 bits (44), Expect = 7.5 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Minus
       528
Query
                AAGCGACCCATGAACGCCTTCATGGTGTGG
                                                  557
                Sbjct
      1885418
                                                  1885389
>ref|NW_001838022.2|Hs11_WGA731_36 Momo sapiens chromosome 11 genomic contig, alternate as
(based on HuRef SCAF_1103279188392)
Length=42354830
                                                            Sort alignments for this subject seq
                                                              E value Score Percent identity
                                                              Query start position Subject star
 Features in this part of subject sequence:
   SRY (sex determining region Y)-box 6 isoform 1
   SRY (sex determining region Y)-box 6 isoform 2
 Score = 50.0 bits (54), Expect = 0.014 Identities = 65/90 (72%), Gaps = 0/90 (0%)
 Strand=Plus/Plus
       522
                 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
Query
                 34920132
                                                                                   34920191
Sbjct
       582
                 ATGGAGCAGTCGCCCGACATGCACAACGCC
Query
                             CTTCAGGCCTTCCCCGACATGCATAACTCC
Sbict
       34920192
                                                   34920221
Features flanking this part of subject sequence:
   33 bp at 5' side: mitogen-activated protein kinase 8 interacting protein 1 13517 bp at 3' side: cryptochrome 2 (photolyase-like)
 Score = 41.0 bits (44), Expect = 7.5 Identities = 35/42 (83%), Gaps = 1/42 (2%)
 Strand=Plus/Minus
Query 1155
                GCCTCCGCCTCCTCGGCAGCCTCCGCAGCGCTCGCG
                 Sbjct
       5001886
Features flanking this part of subject sequence: 1290185 bp at 5' side: mucin 15 199821 bp at 3' side: leucine zipper protein 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG
                                                2082
                 25626780
Sbjct
                                                25626754
>ref|NW_001838468.1|Hs18_WGA1177_36 Memory Bounds Sapiens chromosome 18 genomic contig, alternate a
(based on HuRef SCAF_1103279188038)
Length=7515650
Features in this part of subject sequence: similar to hCG1790759
 Score = 50.0 bits (54), Expect = 0.014 Identities = 35/40 (87%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATGGCaaaaaaaaa
                 1473112
                 TTGTTGTTGTTGTTGTTGTTGAAAAAAAAAAAAAA
Sbjct
```

>ref|NW_001838951.1|Hs5_WGA344_36 💹 Homo sapiens chromosome 5 genomic contig, alternate asse

```
(based on HuRef SCAF_1103279188395)
Length=20933881
```

```
Sort alignments for this subject seq
                                                                                                                                    E value Score Percent identity
                                                                                                                                    Query start position Subject star
  Features flanking this part of subject sequence:
      699382 bp at 5' side: myocyte enhancer factor 2C 378040 bp at 3' side: hypothetical protein
  Score = 50.0 bits (54), Expect = 0.014 Identities = 35/40 (87%), Gaps = 0/40 (0%)
  Strand=Plus/Minus
Query 2056
                                      TTGTTGTTATTGATGTTGTTGATGGCaaaaaaaaa
                                                                                                                                    2095
                                      Sbjct 18105201
                                     TTGTTGTTGTTGTTGTTGATAGAAACAAAAAAA
                                                                                                                                    18105162
  Features flanking this part of subject sequence:
      1347233 bp at 5' side: EGF-like repeats and discoidin I-like domains-containing ... 881684 bp at 3' side: cytochrome c oxidase subunit VIIc precursor
  Score = 44.6 bits (48), Expect = 0.62
  Identities = 33/39 (84%), Gaps = 0/39 (0%)
  Strand=Plus/Plus
Query 2056
                                      TTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAAA
                                      Sbjct 14316178
>ref|NW_001838865.2|Hs2_WGA258_36 Dominion of the same of the same
(based on HuRef SCAF_1103279188138)
Length=7557636
 Features flanking this part of subject sequence: 283252 bp at 5' side: hypothetical protein LOC79843 116307 bp at 3' side: plasminogen activator inhibitor type 1, member 2
  Score = 50.0 bits (54), Expect = 0.014
  Identities = 35/40 (87%), Gaps = 0/40 (0%)
  Strand=Plus/Plus
Query 2047
                                    GACCTGTGATTGTTGTTGATGTTGTTGATGGCAA
                                    GACCTGGGATTTTTGTTGTTGTTGTTGTTGTTGTTGCCAA
Sbjct 1525080
                                                                                                                                1525119
>ref|NT_006576.15|Hs5_6733 MM Homo sapiens chromosome 5 genomic contig, reference assembly
Length=46378398
                                                                                                                               Sort alignments for this subject seq
                                                                                                                                    E value Score Percent identity
                                                                                                                                    Query start position Subject star
  Features flanking this part of subject sequence: 1500958 bp at 5' side: hypothetical protein 319712 bp at 3' side: cadherin 18, type 2 preproprotein
  Score = 50.0 bits (54), Expect = 0.014 Identities = 27/27 (100%), Gaps = 0/27 (0%)
  Strand=Plus/Minus
Query 2056
                                      TTGTTGTTATTGATGTTGTTGATG
                                                                                                      2082
                                     Sbjct 19126380
                                                                                                      19126354
  Features flanking this part of subject sequence:
      2372 bp at 5' side: hypothetical protein 695213 bp at 3' side: hypothetical protein
  Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
```

Strand=Plus/Minus

```
GGGGAGCTGGCGGCGGCGGCTGCTGGGCCTCC 2659
Query 2628
                 Sbjct 1877085
                 GGGGAGCGGCGGCGGCTGCGGCGACTCC
 Features in this part of subject sequence:
   KPL2 protein isoform 1
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2052
                  GTGATTGTTGTTTGTTGTT
                                                 2078
                  Sbjct 35740888
                                                 35740914
>ref|NT_009237.17|Hs11_9394 Memo sapiens chromosome 11 genomic contig, reference assembly
Length=\overline{49571094}
                                                             Sort alignments for this subject seq
                                                               E value Score Percent identity
                                                               Query start position Subject star
 Features in this part of subject sequence:
   SRY (sex determining region Y)-box 6 isoform 2
   SRY (sex determining region Y)-box 6 isoform 1
Score = 50.0 bits (54), Expect = 0.014 Identities = 65/90 (72%), Gaps = 0/90 (0%)
 Strand=Plus/Minus
Query 522
                  \tt CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC
                                                                                    581
                 Sbjct
       14797892
                                                                                    14797833
       582
                  ATGGAGCAGTCGCCCGACATGCACAACGCC
Query
                                                    611
                               CTTCAGGCCTTCCCCGACATGCATAACTCC
Sbjct 14797832
Features flanking this part of subject sequence: 193583 bp at 5' side: leucine zipper protein 2 1060010 bp at 3' side: transmembrane protein 16C
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Plus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                                                 2082
                  Sbjct 24081028 TTGTTGTTGTTGTTGTTGATG
                                                 24081054
 Features flanking this part of subject sequence:
   13517 bp at 5' side: cryptochrome 2 (photolyase-like) 33 bp at 3' side: mitogen-activated protein kinase 8 interacting protein 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 35/42 (83%), Gaps = 1/42 (2%)
 Strand=Plus/Plus
Query 1155
                  GCCTCCGCCTCCGCAGCCTCGGCCTCCGCAGCGCTCGCG
                                  GCTCCGCCTCCTTCGCAGCCGCCCCCTCCTCCGCGC-CGCG
Sbjct 44694540
                                                                 44694580
>ref|NT_007819.16|Hs7_7976 Whomo sapiens chromosome 7 genomic contig, reference assembly
Length=47690382
                                                             Sort alignments for this subject seq
                                                               E value Score Percent identity
                                                               Query start position Subject star
 Features flanking this part of subject sequence:
   627203 bp at 5' side: Sp8 transcription factor isoform 2 15247 bp at 3' side: Sp4 transcription factor
```

```
Score = 50.0 bits (54), Expect = 0.014 Identities = 35/40 (87%), Gaps = 0/40 (0%)
 Strand=Plus/Plus
Query 2056
                 TTGTTGTTGTTGTTGTTGTTGTTAAAAAAAAAAAA
Sbjct 20941542
                                                             20941581
Features in this part of subject sequence:
   zinc finger/RING finger 2
 Score = 44.6 bits (48), Expect = 0.62 Identities = 48/64 (75%), Gaps = 0/64 (0%)
 Strand=Plus/Plus
Query 1143
                 CCCAGCGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGCAGCGCTCGCGGCCCCG
                                                                                  1202
                 CCCAGCGCCTCCGGCGCGCCGCGGCGGCCGCCGGCAGCCCCGGCGGCCCCG
Sbjct
      29814106
                                                                                  29814165
                 GGCA 1206
Query 1203
                  \perp
Sbjct 29814166 CGCA 29814169
 Features flanking this part of subject sequence:
   130830 bp at 5^{\circ} side: T-box transcription factor TBX20 isoform B 249206 bp at 3' side: HERPUD family member 2
 Score = 44.6 bits (48), Expect = 0.62 Identities = 30/34 (88%), Gaps = 0/34 (0%)
 Strand=Plus/Minus
                 CCtttttttCCTCCTCTTTTCCCCTTGCCCCCT
Query 2423
                  Sbjct 34913052 CCTTTTCTTCCTCCTCTTTTCCTCCTCCT
                                                       34913019
Features flanking this part of subject sequence: 627200 bp at 5' side: Sp8 transcription factor isoform 2 15248 bp at 3' side: Sp4 transcription factor
 Score = 42.8 bits (46), Expect = 2.2 Identities = 35/42 (83%), Gaps = 2/42 (4%)
 Strand=Plus/Plus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG--GCaaaaaaaaaa
                  Sbjct 20941539 TTGTTGTTGTTGTTGTTGTTGTTGTTGTTAAAAAAAA 20941580
 Features in this part of subject sequence:
  transformer-2 alpha
 Score = 42.8 bits (46), Expect = 2.2
 Identities = 29/33 (87%), Gaps = 0/33 (0%)
 Strand=Plus/Plus
Query 766
                 CCAACTCCAGCTCCTCGGCCGCCGCCTCCTCCA
       23034796 CCACCTCCACCTCCACCGCCGCCGCCTCCTCA
                                                     23034828
Features in this part of subject sequence:
   sorting nexin 8
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87\%), Gaps = 0/32 (0\%)
 Strand=Plus/Plus
Query 1158
                TCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC
                Sbjct 1842936 TCCGCCTCCTCGTCAGCCTCCGCCTCAGCTGC 1842967
```

Features flanking this part of subject sequence:

```
213509 bp at 5' side: serine/threonine kinase 31 isoform b 239342 bp at 3' side: neuropeptide Y
 Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96\%), Gaps = 0/25 (0\%)
 Strand=Plus/Minus
Query 2055
                 ATTGTTGTTATTGATGTTGTTG
                 Sbjct
       23574476
                 ATTGTTGTTATTGTTGTTGTTG
Features flanking this part of subject sequence: 29183 bp at 5' side: ras related v-ral simian leukemia viral oncogene homolog A
   67365 bp at 3' side: hypothetical protein
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
Query 2053
                 TGATTGTTGTTTGTTGTTGTTG
                 Sbjct 39264011
                 TGATTGTTGTTGTTGTTGTTG
                                              39263985
>ref|NT 010966.13|Hs18 11123 💹 Homo sapiens chromosome 18 genomic contig, reference assembly
Length=33548238
Features in this part of subject sequence:
   similar to hCG1790759
 Score = 50.0 bits (54), Expect = 0.014
 Identities = 35/40 (87%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTGTTGTTGTTGTTGAAAAAAAAAAAAAA
       27513661
                                                            27513622
Sbjct
>ref|NT_010393.15|Hs16_10550 Weak Homo sapiens chromosome 16 genomic contig, reference assembly
Length=25336229
                                                          Sort alignments for this subject seq
                                                            E value Score Percent identity
                                                            Query start position Subject star
 Features flanking this part of subject sequence:
   508 bp at 5' side: ubiquitin specific protease 7 128183 bp at 3' side: hypothetical protein LOC29035
 Score = 50.0 bits (54), Expect = 0.014 Identities = 54/70 (77%), Gaps = 5/70 (7%)
 Strand=Plus/Plus
               TCCCAGCGCCTCGGCCTCCTCGGCAGCCTC----GGCCTCC-GCAGCGCTCGCG
Query
     1142
                                                                              1196
               370729
Sbjct
                                                                               370788
Query 1197
               GCCCCGGGCA 1206
               GCGCCCGGCA
Sbjct
       370789
                           370798
Features in this part of subject sequence:
  poly(A)-specific ribonuclease (deadenylation nuclease)
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2052
                GTGATTGTTGTTATTGATGTTGTT
                                              2078
                    GTGGTTGTTGTTGTTGTTGTT
Sbjct
      5859015
                                              5858989
```

Features flanking this part of subject sequence:

```
71489 bp at 5' side: sodium channel, nonvoltage-gated 1, gamma 61616 bp at 3' side: sodium channel, nonvoltage-gated 1, beta
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                  Sbjct 14611358
                  TTGTTGTTGATGTTGTTGTTG
>ref|NT_005403.16|Hs2_5560 Memory Homo sapiens chromosome 2 genomic contig, reference assembly
Length=84213157
                                                             Sort alignments for this subject seq
                                                               E value Score Percent identity
                                                               Query start position Subject star
 Features flanking this part of subject sequence:
   127128 bp at 5 side: hypothetical protein
   282932 bp at 3' side: hypothetical protein LOC79843
 Score = 50.0 bits (54), Expect = 0.014 Identities = 35/40 (87%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query
       2047
                  GACCTGTGATTGTTGTTGTTGATGTTGTTGATGGCAA
                                                               2086
                  75191620
                  GACCTGGGATTTTTGTTGTTGTTGTTGTTGTTGTTGCCAA
                                                               75191581
Sbjct
 Features flanking this part of subject sequence:
   237306 bp at 5 side: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga...
   10897 bp at 3' side: potassium inwardly-rectifying channel J3
 Score = 42.8 bits (46), Expect = 2.2 Identities = 23/23 (100%), Gaps = 0/23 (0%)
 Strand=Plus/Plus
Query 2241
                 GTTTTGTTTTATTTTGCTTCTTG
                                            2263
                 Sbjct 5753787
                                            5753809
                 GTTTTGTTTTATTTTGCTTCTTG
 Features in this part of subject sequence:
   homeobox D11
Score = 42.8 bits (46), Expect = 2.2 Identities = 28/31 (90%), Gaps = 0/31 (0%)
 Strand=Plus/Minus
Query 1159
                  CCGCCTCCTCGGCAGCCTCGGCCTCCGCAGC
       27181871 CCGCCTCCTCGGCCGCCGCCGCCGCCGCAGC
                                                     27181841
 Features in this part of subject sequence:
   titin isoform N2-A
   titin isoform novex-1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                                                 2082
                  TTGTTGTTGATGTTGTTGTTG
                                                 29758357
Sbjct
       29758383
>ref|NT_006713.14|Hs5_6870 Memo sapiens chromosome 5 genomic contig, reference assembly
Length=42230486
```

```
Features flanking this part of subject sequence:
   699394 bp at 5' side: myocyte enhancer factor 2C
377967 bp at 3' side: hypothetical protein
 Score = 50.0 bits (54), Expect = 0.014 Identities = 35/40 (87%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATGGCaaaaaaaaaaaa
                                                                  2095
                   Sbjct 39413396
                  TTGTTGTTGTTGTTGTTGATAGAAACAAAAAAA
                                                                  39413357
 Features flanking this part of subject sequence:
   1351749 bp at 5' side: EGF-like repeats and discoidin I-like domains-containing ... 881894 bp at 3' side: cytochrome c oxidase subunit VIIc precursor
 Score = 44.6 bits (48), Expect = 0.62 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Plus
Query 2056
                   Sbjct 35626299
                                                                 35626337
 Features flanking this part of subject sequence:
   98714 bp at 5'side: înterleukin 6 signal transducer isoform 2 precursor 25158 bp at 3' side: ankyrin repeat domain 55 isoform 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 30/34 (88%), Gaps = 1/34 (2%)
 Strand=Plus/Minus
Query 2049
                  CCTGTGATTGTTGTTGATGTTGTTGATG
                 Sbjct 5965211
                                                          5965179
>ref|NW_001838061.2|Hs12_WGA770_36 Momo sapiens chromosome 12 genomic contig, alternate as
(based on HuRef SCAF_1103279188362)
Length=32873191
                                                                Sort alignments for this subject seq
                                                                  E value Score Percent identity
                                                                  Query start position Subject star
Features flanking this part of subject sequence: 63961 bp at 5' side: hypothetical protein LOC196477 1181244 bp at 3' side: hypothetical protein
 Score = 46.4 bits (50), Expect = 0.18 Identities = 34/40 (85%), Gaps = 0/40 (0%)
 Strand=Plus/Plus
                   TTGTTGTTATTGATGTTGTTGATGGCaaaaaaaaaaaa
Query 2056
                                                                  2095
                   Sbjct 18088785
                  TTGTTGTTGTTGTTGTTGTTGTTTAAAAAAAAAA
                                                                  18088824
 Features flanking this part of subject sequence:
   4678 bp at 5' side: damage-regulated autophagy modulator 42189 bp at 3' side: N-acetylglucosamine-l-phosphate transferase
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                                                  2082
                  7113244
                 TTGTTGTTATTGTTGTTGTTGTTG
                                                  7113270
 Features flanking this part of subject sequence:
   15027 bp at 5' side: IKK interacting protein isoform 1
   9365 bp at 3' side: solute carrier family 25 member 3 isoform b precursor
```

```
Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
                   TGTGATTGTTGTTGATGTTGTTGATG
Query 2051
                   Sbjct 10374017
                  TGTGTTGTTGTTGTTGTTGTTGTTG
                                                        10374048
 Features flanking this part of subject sequence:
   11252 bp at 5' side: tetraspanin 19 111109 bp at 3' side: solute carrier family 6, member 15 isoform 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2059
                   TTGTTATTGATGTTGTTGATGGCA
                                                   2085
                   Sbjct 23985705
                  TTGTTGTTGTTGTTGTTGATGGCA
                                                   23985679
 Features flanking this part of subject sequence:
   1244859 bp at 5' side: solute carrier family 6, member 15 isoform 2
   505592 bp at 3' side: transmembrane and tetratricopeptide repeat containing 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 29/32 (90%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
                  CCTGT-GATTGTTGTTATTGATGTTGTTG
Query 2049
                                                         2079
                   Sbjct 25350079
                  CCTGTAGTTTGTTGTTGTTGTTGTTG
                                                         25350048
Features flanking this part of subject sequence:
   60181 bp at 5' side: hypothetical protein 36799 bp at 3' side: synaptotagmin I
 Score = 41.0 bits (44), Expect = 7.5 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Minus
Query 2053
                   TGATTGTTGTTGATGTTGTTGATG
                  29504024
Sbjct
>ref|NW_001838006.2|Hs10_WGA715_36 Momo sapiens chromosome 10 genomic contig, alternate as
(based on HuRef SCAF_1103279188397)
Length=24511762
                                                               Sort alignments for this subject seq E value Score Percent identity
                                                                  Query start position Subject star
Features flanking this part of subject sequence: 21875 bp at 5' side: VPS10 domain receptor protein SORCS 3 164826 bp at 3' side: coiled-coil domain containing 147
 Score = 46.4 bits (50), Expect = 0.18 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Plus
Query 2050
                   CTGTGATTGTTGTTGTTGTTG
                                                      2079
                   Sbjct 18620835 CTGTGATTGTTGTTGTTGTTGTTGTTG 18620864
 Features in this part of subject sequence:
   attractin-like 1
 Score = 42.8 bits (46), Expect = 2.2
 Identities = 31/36 (86%), Gaps = 0/36 (0%)
 Strand=Plus/Plus
```

```
Query 2047
                 GACCTGTGATTGTTGTTATTGATGTTGTTGATG
                                                          2082
                Sbjct
      7796118
                                                          7796153
 Features in this part of subject sequence:
   eukaryotic translation initiation factor 3, subunit 10 th...
 Score = 41.0 bits (44),
                          Expect = 7.5
 Identities = 30/34 (88%), Gaps = 1/34 (2%)
 Strand=Plus/Plus
Query 2049
                 CCTGTGATTGTTGTTGATGTTGTTGATG
                 CCTGTG-TTGTTGTTTTTTGTTGTTGTTGTTG
Sbjct
       4199496
                                                        4199528
>ref|NW_001838988.2|Hs6_WGA381_36 🎆 Homo sapiens chromosome 6 genomic contig, alternate asse
(based on HuRef SCAF_1103279187031)
Length=10950630
Features flanking this part of subject sequence: 5780 bp at 5' side: PR domain containing 13 31753 bp at 3' side: cyclin C isoform a
 Score = 46.4 bits (50), Expect = 0.18 Identities = 30/32 (93%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query 2423
                 CCtttt-tttCCTCCTCTTTTCCCCTTGCCC
                 CCTTTTATTTCTTCCCTCTTTTCCCCTTGCCC
Sbjct 6415009
                                                      6414978
>ref|NT_025741.14|Hs6_25897 Web Homo sapiens chromosome 6 genomic contig, reference assembly
Length=61645385
                                                             Sort alignments for this subject seq
                                                               E value Score Percent identity
                                                               Query start position Subject star
 Features flanking this part of subject sequence:
   39819 bp at 5' side: cyclin C isoform b 5780 bp at 3' side: PR domain containing 13
 Score = 46.4 bits (50), Expect = 0.18
 Identities = 30/32 (93%), Gaps = 1/32 (3%)
 Strand=Plus/Plus
Query 2423
                 CCtttt-tttCCTCCTCTTTTCCCCTTGCCC
Sbjct 4218557 CCTTTTATTTCTTCCCTTTTTCCCCTTGCCC
                                                     4218588
Features flanking this part of subject sequence:
44704 bp at 5' side: cell division cycle 2-like 6 (CDK8-like)
15240 bp at 3' side: S-adenosylmethionine decarboxylase 1 isoform 1 precursor
 Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                                                 2082
                  Sbjct 15350472 TTGTTGTTGATGTTGTTGTTGTTG
                                                 15350498
 Features flanking this part of subject sequence:
   536408 bp at 5' side: connexin 43
   415307 bp at 3' side: heat shock transcription factor 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
```

```
26409985
                 TTGTTGTTGTTGTTGTTGTTGATG 26410011
 Features flanking this part of subject sequence:
   422057 bp at 5' side: sterile alpha motif domain containing 5
   356529 bp at 3' side: SAM and SH3 domain containing 1
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2237
                 CTTGGTTTTGTTTTATTTTGCTTCTTG
                                                2263
                  52412078
                 CTTTGTTTTGTTTTATTTTGCTTTTTG
                                                52412104
Sbjct
 Features in this part of subject sequence:
   opioid receptor, mu 1 isoform MOR-10
   phosphoinositide-binding protein PIP3-E
Score = 41.0 bits (44), Expect = 7.5 Identities = 29/32 (90%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATGGCAAA
                                                      2087
                  TTGTTGTTGTTGTTGTTGA-GGCAAA
       58617258
                                                      58617228
Sbict
>ref|NT_113898.1|Hs6_111617 💹 Homo sapiens chromosome 6 genomic contig, reference assembly
Length=1305230
 Features flanking this part of subject sequence:
   539 bp at 5' side: similar to HGC6.4
105 bp at 3' side: similar to myeloid/lymphoid or mixed-lineage leukemia (tr...
 Score = 46.4 bits (50), Expect = 0.18 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Minus
Query 1155
               GCCTCCGCCTCCTCGGCAGCCTCCGCAGC
                GCCTCCGCCTCCGCGGCTGCCTCCGCGGC
Sbjct 814424
                                                       814390
>ref|NT_007302.13|Hs6_7459 Weak Homo sapiens chromosome 6 genomic contig, reference assembly
Length=2236975
 Features flanking this part of subject sequence:
   539 bp at 5' side: hypothetical protein LOC653483
   105 bp at 3' side: myeloid/lymphoid or mixed-lineage leukemia (trithorax hom...
Score = 46.4 bits (50), Expect = 0.18 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Minus
Query 1155
               GCCTCCGCCTCCTCGGCAGCCTCCGCAGC
                ĠĊĊŢĊĊĠĊĊŢĊĊĠĊĠĠĊŢĠĊĊŢĊĊĠĊĠĠĊ
>ref|NT_030059.12|Hs10_30314 We Homo sapiens chromosome 10 genomic contig, reference assembly
Length=44617998
                                                            Sort alignments for this subject seq
                                                              E value Score Percent identity
                                                              Query start position Subject star
Features flanking this part of subject sequence: 164871 bp at 5' side: coiled-coil domain containing 147
   21898 bp at 3' side: VPS10 domain receptor protein SORCS 3
 Score = 46.4 bits (50), Expect = 0.18 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Minus
```

```
Query 2050
                 CTGTGATTGTTGTTATTGATGTTGTTG
                Sbjct 25127714
                                                 25127685
 Features in this part of subject sequence:
  attractin-like 1
 Score = 42.8 bits (46), Expect = 2.2 Identities = 31/36 (86%), Gaps = 0/36 (0%)
 Strand=Plus/Minus
Query 2047
                 GACCTGTGATTGTTGTTGTTGATGTTGTTGATG
                 GACCTATGCTTGTTGTTGTTGTTGTTGTTGTTG
Sbjct
       35956938
                                                        35956903
Features flanking this part of subject sequence:
48094 bp at 5' side: protein phosphatase 1, regulatory (inhibitor) subunit 3C
117589 bp at 3' side: tankyrase, TRF1-interacting ankyrin-related ADP-ribose po...
 Score = 41.0 bits (44), Expect = 7.5 Identities = 33/40 (82%), Gaps = 0/40 (0%)
 Strand=Plus/Plus
Query 2043
                 GGGCGACCTGTGATTGTTGTTATTGATGTTGTTGATG
                       Sbjct 12189336
                 GGGCTTCCTGTTGTTGTTGTTGTTGTTGTTGTTG
                                                            12189375
 Features in this part of subject sequence:
   eukaryotic translation initiation factor 3, subunit 10 th...
 Score = 41.0 bits (44),
                         Expect = 7.5
 Identities = 30/34 (88%), Gaps = 1/34 (2%)
 Strand=Plus/Minus
Query 2049
                 CCTGTGATTGTTGTTGTTGATG
                 Sbjct
>ref|NW_001838769.1|Hs2_WGA162_36 🎆 Homo sapiens chromosome 2 genomic contig, alternate asse
(based on HuRef SCAF_1103279188433)
Length=57109151
                                                          Sort alignments for this subject seq
                                                            E value Score Percent identity
                                                            Query start position Subject star
 Features in this part of subject sequence:
   neurexin 1 isoform alpha precursor
 Score = 44.6 bits (48), Expect = 0.62 Identities = 26/27 (96%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2053
                 TGATTGTTGTTTGTTGTTG
                 Sbjct 20778224 TGATTGTTGTTGTTGTTGTTG
                                              20778198
Features in this part of subject sequence:
  hypothetical protein
 Score = 42.8 bits (46), Expect = 2.2 Identities = 66/91 (72%), Gaps = 9/91 (9%)
 Strand=Plus/Plus
                GGGCGGCGTGGGCCGGGACCCGACCCCTGGGCCTGTACGAGGAGGAG
Query 1277
                                                                               1334
                GGGCGGCGGG-GCGGGCGCGCGGGGGACTCACTGGGGGCGG-----GGCGGAG
      7734878
Sbjct
                                                                               7734930
      1335
                GGCGCGGCTGCTCGCCCGACGCGCCCAGCC
Query
                7734931
                                                  7734961
Sbjct
```

```
Features in this part of subject sequence:
   sterolin 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Plus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                                                  2082
                   Sbjct 13885678 TTGTTGTTATTGTTGTTGTTGTTG
                                                  13885704
 Features flanking this part of subject sequence:
   23818 bp at 5' side: M-phase phosphoprotein 10 14630 bp at 3' side: poly(A) binding protein interacting protein 2B
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                                                  2082
                   Sbjct 41233894 TTGTTGTTATTGTTGTTGTTGCTG
                                                  41233868
 Features flanking this part of subject sequence:
   16873 bp at 5' side: STAM binding protein 23234 bp at 3' side: actin, gamma 2 propeptide
 Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGA
                   Sbjct 43937347
                  TTGTTGTTATTGTTGTTGTTGA
                                                43937323
>ref|NW_001838115.2|Hs14_WGA824_36 W Homo sapiens chromosome 14 genomic contig, alternate as
(based on HuRef SCAF_1103279188327)
Length=8970161
                                                              Sort alignments for this subject seq
                                                                 E value Score Percent identity
                                                                 Query start position Subject star
 Features in this part of subject sequence:
   REST corepressor 1
 Score = 44.6 bits (48),
                           Expect = 0.62
 Identities = 35/42 (83%), Gaps = 0/42 (0%)
 Strand=Plus/Minus
Query 1148
                 CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGCAGC
1645692
Features flanking this part of subject sequence: 73361 bp at 5' side: SET domain containing 3 isoform b 65304 bp at 3' side: B-cell CLL/lymphoma 11B isoform 2
Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96\%), Gaps = 0/25 (0\%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTATTGATGTTGTTGA
                                              2080
                 4895427
                                               4895403
Sbjct
>ref|NW_001838461.1|Hs18_WGA1170_36 💹 Homo sapiens chromosome 18 genomic contig, alternate a
(based on HuRef SCAF_1103279188344)
Length=10560353
 Features flanking this part of subject sequence:
```

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52573 bp at 5' side: zinc finger protein 161 homolog 48166 bp at 3' side: erythrocyte membrane protein band 4.1-like\ 3
 Score = 44.6 bits (48), Expect = 0.62 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
Query 2050
                   CTGTGATTGTTGTTATTGATGTTGTTGAT 2081
                          CTGTTGTTGTTGTTGTTGTTGAT
Sbjct
        5299965
>ref|NW 001838768.1|Hs2 WGA161 36 💹 Homo sapiens chromosome 2 genomic contig, alternate asse
(based on HuRef SCAF_1103279188306)
Length=8993619
 Features flanking this part of subject sequence: 9750 bp at 5' side: similar to hCG1783917
   35597 bp at 3' side: ATPase family, AAA domain containing 2B
 Score = 44.6 bits (48), Expect = 0.62 Identities = 35/42 (83%), Gaps = 0/42 (0%)
 Strand=Plus/Plus
Query 2041
                   AGGGGCGACCTGTGATTGTTGTTATTGATGTTGTTGATG
                   Sbjct 2769192
                   AGGTGGGACCTTTCATTGTTGTTGTTGTTGTTGTTGTTG
                                                                         2769233
>ref|NW_001838987.1|Hs6_WGA380_36 Weak Homo sapiens chromosome 6 genomic contig, alternate asse
(based on HuRef SCAF_1103279188274B)
Length=25130961
                                                                     Sort alignments for this subject seq
                                                                       E value Score Percent identity
                                                                       Query start position Subject star
 Features flanking this part of subject sequence:
   673617 bp at 5' side: similar to OTTHUMP00000016822 14999 bp at 3' side: similar to hCG1652647
 Score = 44.6 bits (48), Expect = 0.62 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
Query 2056
                    TTGTTGTTATTGATGTTGTTGATGGCAAA
                    Sbjct 16521782
 Features flanking this part of subject sequence: 877536 bp at 5' side: hypothetical protein 56773 bp at 3' side: similar to PRO2122
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                    TTGTTGTTATTGATGTTGTTGATG
                                                       2082
                    Sbjct 11600965
>ref|NW_001838928.2|Hs5_WGA321_36 WHomo sapiens chromosome 5 genomic contig, alternate asse
(based on HuRef SCAF_1103279188369)
Length=3866709
 Features flanking this part of subject sequence: 318147 bp at 5' side: cadherin 18, type 2 preproprotein 1493882 bp at 3' side: hypothetical protein
 Score = 44.6 bits (48), Expect = 0.62 Identities = 26/27 (96%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
                   TTGTTGTTATTGATGTTGTTGATG 2082
Query 2056
```

```
Sbjct 2312131
                TTGTTGTTATTGATGTTGTTGTTG
                                              2312157
>ref|NW_001838915.1|Hs4_WGA308_36 💹 Homo sapiens chromosome 4 genomic contig, alternate asse
(based on HuRef SCAF_1103279188399)
Length=43867763
                                                           Sort alignments for this subject seq
                                                             E value Score Percent identity
                                                             Query start position Subject star
Features in this part of subject sequence:
   calcium/calmodulin-dependent protein kinase II delta isof...
   calcium/calmodulin-dependent protein kinase II delta isof...
 Score = 44.6 bits (48), Expect = 0.62 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
Query 2051
                 TGTGATTGTTGTTGATGTTGTTGATG
                 38913468 TGTTATTGTTGTTGTTGTTGTTGTTGTTG
                                                    38913437
Sbjct
 Features flanking this part of subject sequence:
   133705 bp at 5' side: protein kinase, cGMP-dependent, type II 89301 bp at 3' side: RasGEF domain family, member 1B
Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
Query 2051
                TGTGATTGTTATTGATGTTGTTGATG 2082
                Sbjct 6765249 TGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
Features in this part of subject sequence:
  kelch-like 8
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2053
                 TGATTGTTGTTGTTGTTG
                                               2079
                 Sbjct 12614178 TGAGTGTTGTTATTGTTGTTGTTG
                                               12614204
 Features flanking this part of subject sequence:
   29889 bp at 5' side: protein phosphatase 1K (PP2C domain containing) 70965 bp at 3' side: hect domain and RLD 6
 Score = 41.0 bits (44), Expect = 7.5
 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Plus
Query 2055
                 ATTGTTGTTATTGATGTTGTTG
                                            2079
                 Sbjct 13742614 ATTGTTGTTATTGTTGTTGTTG
                                            13742638
 Features flanking this part of subject sequence:
   278276 bp at 5' side: hypothetical protein 1070253 bp at 3' side: hypothetical protein LOC132720
 Score = 41.0 bits (44), Expect = 7.5
 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query 2055
                 ATTGTTGTTATTGATGTTGTTG
                                             2079
                 ATTGTTGTTATTGATGCTGTTGTTG
Sbjct 36489587
Features flanking this part of subject sequence:
```

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829674 bp at 5' side: translocation associated membrane protein 1-like 1 140202 bp at 3' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3
 Score = 41.0 bits (44), Expect = 7.5 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Plus
Query 2053
                  TGATTGTTGTTGATGTTGTTGATG
                     Sbjct
       43331849
                  TGTTTGTTGTTGTTGTTGTTGCTG
>ref|NW 001838878.1|Hs3 WGA271 36 💹 Homo sapiens chromosome 3 genomic contig, alternate asse
(based on HuRef SCAF_1103279188187)
Length=20655341
                                                             Sort alignments for this subject seq
                                                               E value Score Percent identity
                                                               Query start position Subject star
 Features in this part of subject sequence:
   roundabout 1 isoform a
 Score = 44.6 bits (48), Expect = 0.62 Identities = 32/37 (86%), Gaps = 0/37 (0%)
 Strand=Plus/Plus
Querv
       2046
                  CGACCTGTGATTGTTGTTGTTGATGTTGTTGATG
                  CGAACTGTGTTGTTGTTGTTGTTGTTGTTG
       12950732
                                                            12950768
Sbjct
 Features flanking this part of subject sequence:
   605382 bp at 5 side: roundabout 1 isoform b 1368845 bp at 3 side: hypothetical protein
 Score = 41.0 bits (44), Expect = 7.5 Identities = 27/30 (90%), Gaps = 0/30 (0%)
                          Expect = 7.5
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATGGCA
                  TTGTTGTTGTTGTTGTTGATGCCA
Sbjct 13425064
                                                    13425035
>ref|NW_001838953.2|Hs5_WGA346_36 Momo sapiens chromosome 5 genomic contig, alternate asse
(based on HuRef SCAF_1103279188146)
Length=16305437
 Features in this part of subject sequence:
   transmembrane protein 173
Score = 44.6 bits (48), Expect = 0.62 Identities = 30/34 (88%), Gaps = 0/34 (0%)
 Strand=Plus/Plus
Query 2049
                  CCTGTGATTGTTGTTGTTGATG
                  CCTGTGTTGTTGTTGTTGTTGTTGTTGTTG
>ref|NT_026437.11|Hs14_26604 Memo sapiens chromosome 14 genomic contig, reference assembly
Length=88290585
                                                             Sort alignments for this subject seq
                                                               E value Score Percent identity
                                                               Query start position Subject star
 Features in this part of subject sequence:
   REST corepressor 1
 Score = 44.6 bits (48), Expect = 0.62 Identities = 35/42 (83%), Gaps = 0/42 (0%)
 Strand=Plus/Plus
                  CGCCTCGGCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189
```

Query 1148

```
CGCCTCGGGCGCCGCCTCCTCAGCCTCGGCCGCCGC
                                                                        84059152
Sbjct 84059111
 Features flanking this part of subject sequence:
   3679 bp at 5' side: olfactory receptor, family 11, subfamily H, member 1 171138 bp at 3' side: protein expressed in prostate, ovary, testis, and placent...
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG
                  TTGTTGTTGATGTTGTTGTTG
Sbjct 382279
Features flanking this part of subject sequence:
44156 bp at 5' side: hypothetical protein
412677 bp at 3' side: olfactory receptor, family 4, subfamily Q, member 3
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                 TTGTTGTTATTGATGTTGTTGATG
                  Sbjct 802724
                 TTGTTGTTGATGTTGTTGTTG
 Features flanking this part of subject sequence: 418658 bp at 5' side: hypothetical protein
   38175 bp at 3' side: olfactory receptor, family 4, subfamily Q, member 3
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATG
                   Sbjct 1177226
                   TTGTTGTTGATGTTGTTGTTG
 Features flanking this part of subject sequence: 1557415 bp at 5' side: MAM domain containing 1 886142 bp at 3' side: ribosomal protein S29 isoform 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                    TTGTTGTTATTGATGTTGTTGATG
                                                     2082
                    TTGTTGTTGATGTTGTTGTTG
Sbjct 30158138
                                                      30158112
 Features flanking this part of subject sequence:
   50279 bp at 5' side: fermitin family homolog 2 45895 bp at 3' side: DDHD domain containing 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
Query 2056
                    TTGTTGTTATTGATGTTGTTGATG
                    Sbjct
        34467341
                    TTGTTGTTGTTGTTGTTGATG
                                                      34467315
>ref|NT_016354.18|Hs4_16510 Memo sapiens chromosome 4 genomic contig, reference assembly
Length=92123751
                                                                    Sort alignments for this subject seq
                                                                      E value Score Percent identity
```

Features in this part of subject sequence:

Query start position Subject star

```
calcium/calmodulin-dependent protein kinase II delta isof...
   calcium/calmodulin-dependent protein kinase II delta isof...
 Score = 44.6 bits (48), Expect = 0.62 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
Query 2051
                   TGTGATTGTTGTTGATGTTGTTGATG
                   TGTTATTGTTGTTATTGTTGTTGTTGTTG
Sbjct
       38971724
Features flanking this part of subject sequence: 133593 bp at 5' side: protein kinase, cGMP-dependent, type II
   89097 bp at 3' side: RasGEF domain family, member 1B
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
Query 2051
                  TGTGATTGTTGTTGATGTTGTTGATG 2082
                  Sbjct 6807515
                 TGTGTTTGTTGTTGTTGTTGTTGTTGTTG 6807546
Features in this part of subject sequence:
   kelch-like 8
Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Plus
                   TGATTGTTGTTATTGATGTTGTTG
Query 2053
                                                   2079
                   Sbjct 12656097 TGAGTGTTGTTGTTGTTGTTGTTG
                                                   12656123
Features flanking this part of subject sequence:
   29879 bp at 5' side: protein phosphatase 1K (PP2C domain containing) 70436 bp at 3' side: hect domain and RLD 6
 Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Plus
                   ATTGTTGTTATTGATGTTGTTG
Query 2055
                   11111111111111
Sbjct 13777335 ATTGTTGTTGTTGTTGTTGTTG
                                                13777359
Features in this part of subject sequence:
   hypothetical protein LOC54848
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATGGCAAA
                      Sbjct 31046853
                  TTTTTGTTGTTGTTGTTGTTGTTGGCAAA
Features flanking this part of subject sequence: 278486 bp at 5' side: hypothetical protein 1070062 bp at 3' side: hypothetical protein LOC132720
 Score = 41.0 bits (44), Expect = 7.5 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query 2055
                   ATTGTTGTTATTGATGTTGTTG
                   Sbjct 36544821 ATTGTTGTTATTGATGCTGTTGTTG
                                                 36544797
 Features in this part of subject sequence:
   ankyrin 2 isoform 1
```

```
ankyrin 2 isoform 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                    TTGTTGTTATTGATGTTGTTGATG
                   Sbjct 38574052
                                                     38574026
 Features flanking this part of subject sequence: 828203 bp at 5' side: translocation associated membrane protein 1-like 1
   140285 bp at 3' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3
 Score = 41.0 bits (44), Expect = 7.5 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Plus
Query 2053
                    TGATTGTTGTTGATGTTGTTGATG 2082
                    TGTTTGTTGTTGTTGTTGTTGCTG 43382926
Sbjct 43382897
 Features flanking this part of subject sequence: 859109 bp at 5' side: hypothetical protein 1066931 bp at 3' side: hypothetical protein
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
Query 2056
                    TTGTTGTTATTGATGTTGTTGATG
                                                     2082
                    Sbjct 56126973 TTGTTGTTGTTGTTGTTGTTGATG
                                                     56126947
Features flanking this part of subject sequence: 323925 bp at 5' side: protocadherin 10 isoform 2 precursor 1467518 bp at 3' side: similar to Ubiquinol-cytochrome c reductase, complex III ...
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
                    TGTGATTGTTGTTGATGTTGTTGATG
Query 2051
                    Sbjct 58946089 TGTGATTGTTGTTGTTGTTGTTGTTGTTG
                                                           58946058
 Features in this part of subject sequence:
   similar to FRAS1-related extracellular matrix protein 3
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92\%), Gaps = 0/27 (0\%)
 Strand=Plus/Minus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATG 2082
                    Sbjct 69094402 TTGTTGTTGTTGATGTTGTTGTTG
 Features flanking this part of subject sequence:
   39101 bp at 5' side: peptidylprolyl isomerase D 6793 bp at 3' side: hypothetical protein LOC57600
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
Query 2051
                    TGTGATTGTTGTTGATGTTGTTGATG
                    TGTGTTGTTGTTGTTGTTGTTGTTGTTG
Sbjct 84231719
                                                           84231688
 Features flanking this part of subject sequence:
   462638 bp at 5' side: membrane-associated RING-CH protein I
```

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120826 bp at 3' side: acidic nuclear phosphoprotein 32C
 Score = 41.0 bits (44), Expect = 7.5 Identities = 33/40 (82%), Gaps = 0/40 (0%)
 Strand=Plus/Minus
Query 2043
                  GGGCGACCTGTGATTGTTGTTATTGATGTTGTTGATG
                  GGGCTACTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
Sbjct 89545480
                                                                89545441
>ref|NT_023935.17|Hs9_24091 WHOmo sapiens chromosome 9 genomic contig, reference assembly
Length=21507948
                                                              Sort alignments for this subject seq
                                                                E value Score Percent identity
                                                                Query start position Subject star
Features flanking this part of subject sequence: 383166 bp at 5' side: transducin-like enhancer protein 4 1475853 bp at 3' side: transducin-like enhancer protein 1
Score = 44.6 bits (48), Expect = 0.62 Identities = 33/38 (86\%), Gaps = 2/38 (5\%)
 Strand=Plus/Plus
Query 2059
                  TTGTTATTGATGTTGTTGATGGCaaaaaaaaaaaa 2096
      11887792
 Features flanking this part of subject sequence:
   534 bp at 5' side: growth arrest-specific 1 164983 bp at 3' side: similar to hCG1817457
 Score = 44.6 bits (48), Expect = 0.62
 Identities = 49/64 (76%), Gaps = 5/64 (7%)
 Strand=Plus/Plus
                  GGCGCGGACTCCCAGCG---CCTCGGCCTCCGCCTCCTCGGCAGCCTCCGCAGC
Query 1133
                                                                                     1189
                  ĠĠĊĊĊĠĠĊĊĠĊĊĊĊĠĊĠŦĊĊĊŤĊĊĊĊŤĊĊĠĊĆ~~ĊĠĊĠĠĊĂAĊĊĊĠĠĊĊŤĊĊĠĊĀĠA
       18726760
                                                                                     18726817
Sbjct
Query 1190
                  GCTC
                       1193
Sbjct 18726818 GCTC
                       18726821
Features flanking this part of subject sequence: 705126 bp at 5' side: transducin-like enhancer protein 4
   1153902 bp at 3' side: transducin-like enhancer protein 1
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                  TTGTTGTTATTGATGTTGTTGATG
                                                  2082
                  TTGTTGTTGTTGTTGTTGATG
Sbjct 12209743
                                                  12209717
>ref|NT_008470.18|Hs9_8627 Web Homo sapiens chromosome 9 genomic contig, reference assembly
Length=40394265
                                                              Sort alignments for this subject seq
                                                                E value Score Percent identity
                                                                Query start position Subject star
 Features in this part of subject sequence:
   KIAA0368 protein
 Score = 44.6 bits (48), Expect = 0.62 Identities = 27/29 (93%), Gaps = 0/29 (0%)
 Strand=Plus/Plus
Query 1000
                  AGCTCATCCTGGCAGGCGGCGGCGGC
```

```
21566991 AGCTCATCCTGGGAGGCGGAGGCGGCC 21567019
Features in this part of subject sequence:
   DAB2 interacting protein isoform 1
Score = 42.8 bits (46), Expect = 2.2 Identities = 39/49 (79\%), Gaps = 3/49 (6\%)
 Strand=Plus/Plus
Query 298
                CGGCGGCCGCC---GCGAGGGTGTGAGCGCGCGTGGGCGCCCGCCGAGC
                                                                   343
                 31735190
Sbjct 31735142
Features in this part of subject sequence:
  paralemmin 2 isoform b
  paralemmin 2 isoform a
Score = 41.0 bits (44), Expect = 7.5 Identities = 34/41 (82%), Gaps = 2/41 (4%)
 Strand=Plus/Plus
                Query 2056
Sbjct 19981612
                TTGTTGTTATTGTTGTTGTCGTT--TAAGAAAAAAAA
                                                           19981650
Features in this part of subject sequence:
  Ral GEF with PH domain and SH3 binding motif 1
Score = 41.0 bits (44), Expect = 7.5
 Identities = 30/35 (85%), Gaps = 0/35 (0%)
 Strand=Plus/Plus
Query 2048
                                                     2082
                ACCTGTGATTGTTGTTGATGTTGTTGATG
                        37143991 ACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
Sbjct
>ref|NT_022459.14|Hs3_22615 Momo sapiens chromosome 3 genomic contig, reference assembly
Length=24211711
                                                        Sort alignments for this subject seq
                                                          E value Score Percent identity
                                                          Query start position Subject star
Features in this part of subject sequence:
  roundabout 1 isoform a
Score = 44.6 bits (48), Expect = 0.62 Identities = 32/37 (86%), Gaps = 0/37 (0%)
 Strand=Plus/Plus
Query 2046
                CGACCTGTGATTGTTGTTATTGATGTTGTTGATG
                Sbjct 12905511
Features flanking this part of subject sequence: 33219 bp at 5' side: roundabout 1 isoform a 1369909 bp at 3' side: hypothetical protein
Score = 41.0 bits (44), Expect = 7.5 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Minus
Query 2056
                TTGTTGTTATTGATGTTGTTGATGGCA
                                                2085
                Sbjct 13379166
>ref|NT_032977.8|Hs1_33153 MM Homo sapiens chromosome 1 genomic contig, reference assembly
Length=73835825
                                                        Sort alignments for this subject seq
                                                          E value Score Percent identity
```

Query start position Subject star

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Features flanking this part of subject sequence: 216269 bp at 5' side: leucine rich repeat containing 8 family, member C 1792 bp at 3' side: leucine rich repeat containing 8 family, member D
 Score = 44.6 bits (48), Expect = 0.62 Identities = 26/27 (96\%), Gaps = 0/27 (0\%)
 Strand=Plus/Plus
Query 2768
                  GGTTTCGGaaaaaaaaaaaaaaaaaaaaaaa 2794
                   Sbjct 60368729 GGTTTCGGAAAAAAAAAAAAAAAAAA
                                                  60368755
 Features flanking this part of subject sequence:
   30984 bp at 5' side: Cbp/p300-interacting transactivator, with Glu/Asp-rich ca... 90153 bp at 3' side: CTP synthase
 Score = 42.8 bits (46), Expect = 2.2 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Minus
                  TTGTTGTTATTGATGTTGTTGATGG 2083
Query 2056
Sbjct 11330728 TTGTTGTTGTTGTTGTTGTTGATGG
 Features flanking this part of subject sequence:
   64368 bp at 5' side: discs, large (Drosophila) homolog-associated protein 3 6709 bp at 3' side: hypothetical protein
 Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus
Query 2051
                 TGTGATTGTTATTGATGTTGTTGATG 2082
                  Sbjct 5407270
                 TGTTATTGTTGTTGTTGCTGTTGTTGTTGTTG 5407301
 Features in this part of subject sequence:
   eukaryotic translation initiation factor 2B, subunit 3 gamma
Score = 41.0 bits (44), Expect = 7.5 Identities = 32/36 (88%), Gaps = 2/36 (5%)
 Strand=Plus/Minus
Query 2244
                  TTGTTTTATTTTG-CTTCTTGGTCAAGAAAGGAGGG 2278
                   Sbjct 15312647 TTGTTTTATTTTGTTTTCTTGG-CAAGAGAGGAGGG 15312613
Features in this part of subject sequence:
   ubiquitin specific protease 24
Score = 41.0 bits (44), Expect = 7.5 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATGGCAAA 2087
                   Sbjct 25513245 TTGTTGTTGTTGTTGTTGTTGTTGTCAAA 25513214
Features in this part of subject sequence:
   DnaJ (Hsp40) homolog, subfamily C, member 6
 Score = 41.0 bits (44), Expect = 7.5
 Identities = 36/44 (81%), Gaps = 1/44 (2%)
 Strand=Plus/Plus
Query 2049
                  CCTGTGATTGTTGTTGATGTTGTTGATGGCAAAAAAA
                                                                      2092
                             Sbjct 35774590 CCTGTG-TAATTTTTGTTGTTGTTGTTGTTGTTGTTGGGAAAAAAA
                                                                      35774632
```

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Features in this part of subject sequence:
   adenylate kinase 5 isoform 1 adenylate kinase 5 isoform 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2053
                   TGATTGTTGTTTGTTG
                                                   2079
                   Sbjct 47884298 TGTTTGTTGTTGTTGTTGTTGTTG
                                                   47884324
 Features flanking this part of subject sequence:
   20976 bp at 5' side: guanylate binding protein 1, interferon-inducible, 67kD 23939 bp at 3' side: guanylate binding protein 2, interferon-inducible
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATG
                                                   2082
                   Sbjct 59521838 TTGTTGTTATTGTTGTTGTTGTTG
                                                   59521812
 Features flanking this part of subject sequence:
   1219349 bp at 5' side: similar to hCG2040669 184274 bp at 3' side: polypyrimidine tract binding protein 2
 Score = 41.0 bits (44), Expect = 7.5 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus
Query 2056
                   TTGTTGTTATTGATGTTGTTGATG
                   Sbjct 66975040
                  TTGTTGTTATTGTTGTTGTTGTTG
                                                   66975066
>ref|NT_010859.14|Hs18_11016 💹 Homo sapiens chromosome 18 genomic contig, reference assembly
Length=15400898
 Features flanking this part of subject sequence:
   37804 bp at 5' side: hypothetical protein 48190 bp at 3' side: erythrocyte membrane protein band 4.1-like 3
 Score = 44.6 bits (48), Expect = 0.62 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus
Query 2050
                  CTGTGATTGTTGTTATTGATGTTGTTGAT
                        CTGTTGTTGTTGTTGTTGTTGTTGAT
Sbjct 5336492
  Database: human build 36.3 reference assembly genomic scaffolds
    Posted date: Apr 16, 2008 7:40 PM
  Number of letters in database: 1,523,044,440
  Number of sequences in database: 49,942
Lambda
            K
            0.408
                       0.912
   0.634
Gapped
Lambda
            K
   0.634
            0.408
                       0.912
Matrix: blastn matrix:2 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 49942
Number of Hits to DB: 5820376
Number of extensions: 423311
Number of successful extensions: 1102
```

```
Number of sequences better than 10: 52
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 1085
Number of HSP's successfully gapped: 58
Length of query: 2797
Length of database: 5818011736
Length adjustment: 35
Effective length of query: 2762
Effective length of database: 5816263766
Effective search space: 16064520521692
Effective search space used: 16064520521692
A: 0
X1: 22 (20.1 bits)
X2: 33 (29.8 bits)
X3: 110 (99.2 bits)
S1: 36 (33.7 bits)
S2: 44 (41.0 bits)
```